

CESS DE # 204404

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Scientific and Technical Information Center

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SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 10-12-06
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/604926
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Bio Informatically

Inventors (please provide full names): Bentwich et al

Earliest Priority Date: 8/27/03

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please Search Seq ID No. 1931
limit to 120 NTS.

Seq ID No: 4539
Size limit to 30 NTS.

1931-61NA
4539-19NA

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:31:43 ; Search time 2388 Seconds

(without alignments)
1428.425 Million cell updates/sec

Title: US-10-604-926A-1931

Perfect score: 61
Sequence: 1 agctgcctctctctctcc.....gggagagggggtgggtgct 61

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 1484138

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	96.7	99	10 F24424	F24424 HSPD10720 H
2	43.4	71.1	83	7 AW009266	AW009266 WS80a06.x
3	27.6	45.2	77	9 DN374929	DN374929 LIB38529
4	25.6	42.0	103	1 AA731471	AA731471 nz98f08.5
5	24.4	40.0	82	13 CW33527	CW33527 104_835.1
6	24.2	40.0	84	13 CW335786	CW335786 104_834.1
7	24.2	39.7	70	13 DU329889	DU329889 109848604
8	23.6	38.7	69	13 CW130949	CW130949 104_513.1
9	23.6	38.7	78	13 CW189398	CW189398 104_610.1
10	23.6	38.7	78	13 CW189398	CW189398 104_610.1
11	23.6	38.7	82	13 CW33527	CW33527 104_835.1
12	23.4	38.4	91	11 BH415834	BH415834 1007045A0
13	23.4	38.4	119	3 BP112776	BP112776 BP112776
14	23.2	38.0	55	9 DN373872	DN373872 LIB38528
15	23.2	38.0	68	14 CR147982	CR147982 Forward's
16	23	37.7	115	1 AI858529	AI858529 w139h03.x
17	23	37.7	120	7 BE082457	BE082457 RC5-BT063
18	22.8	37.4	73	1 AI718969	AI718969 as50f01.x
19	22.8	37.4	98	5 CF197798	CF197798 maj40b02.

20	22.8	37.4	111	13 CW189218	CW189218 104_610.1
21	22.6	37.0	112	9 DN440660	DN440660 LIB5337-0
22	22.6	37.0	114	2 BF832254	BF832254 PM3-HT092
23	22.6	37.0	118	1 AI589396	AI589396 tr61h10.x
24	22.4	36.7	99	10 F24424	F24424 HSPD10720 H
25	22.4	36.7	117	12 CG566740	CG566740 OST192605
26	22.2	36.4	76	12 CG668667	CG668667 OST458079
27	22.2	36.4	98	13 CL279855	CL279855 Ggal_142c
28	22.2	36.4	107	8 CO529989	CO529989 3530_1.19
29	22.2	36.4	113	7 AW028147	AW028147 wv26f08.x
30	22.2	36.4	115	5 CD696564	CD696564 EST13087
31	22.2	36.4	119	1 AI824210	AI824210 wj36b05.x
32	22.2	36.4	119	14 CR001418	CR001418 Forward's
33	22	36.1	70	14 DX107181	DX107181 644_2_141
34	22	36.1	70	14 DX107181	DX107181 644_2_141
35	22	36.1	72	14 CR194047	CR194047 Reverse s
36	22	36.1	89	14 CR037539	CR037539 Reverse s
37	22	36.1	94	8 CO887582	CO887582 BovGen.15
38	21.8	35.7	83	11 AZ639232	AZ639232 IM0499M06
39	21.8	35.7	110	5 CI299381	CI299381 CI299381
40	21.8	35.7	117	7 BE487605	BE487605 176447 BA
41	21.8	35.7	118	1 AA646954	AA646954 v138d09.r
42	21.8	35.7	120	5 CI297065	CI297065 CI297065
43	21.6	35.4	101	5 CD945340	CD945340 RDX_27 Ge
44	21.6	35.4	101	8 CO824350	CO824350 LM_GB5_00
45	21.6	35.4	112	3 BU754334	BU754334 UI-1-BB1p

ALIGNMENTS

RESULT 1
F24424
LOCUS HSPD10720 HM3 Homo sapiens cDNA clone s400009E12, mRNA sequence. 99 bp mRNA linear EST 13-MAY-1999
DEFINITION F24424
ACCESSION F24424
VERSION F24424.1 GI:4810050
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 99)
Landranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A., Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.
Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization
Genome Res. 6 (1), 35-42 (1996)
8681137
Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
http://group.bio.unipd.it.
Location/Qualifiers
1..99
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="s400009E12"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/clone_lib="HM3"
/note="Vector: pcDNAII (Invitrogen); Site 1: BstXI; Site 2: NotI; The library was constructed by G. Landranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer (5'-biotin-AACCGCTCGAGCGCGCTTTTCTTTTCTTTT-3'). The ds cDNA was sonicated and size-selected in the range.

350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pCDNA1 vector."

ORIGIN

Query Match 96.7%; Score 59; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCCCTCTCTTCTCCCTCACACTACAGCCCTGTTGGGGAGAGGGGGTGGTGC 59
|||||
Db 41 AGCTGCCCTCTCTTCTCCCTCACACTACAGCCCTGTTGGGGAGAGGGGGTGGTGC 99
|||||

RESULT 2

AW009266/c
LOCUS
DEFINITION w80a06.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504242 3',
mRNA sequence.
ACCESSION AW009266
VERSION AW009266.1 GI:5858044
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 83)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1204 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 82.

FEATURES

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1. .83
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2504242"
/sex="pooled"
/tissue type="colon"
/lab host="DH10B"
/clone lib="NCI CGAP Co3"
/note="Vector: pTT3D-PacI; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was prepared from 12 pooled bulk tumor
samples and primed with a Not I - oligo(dT) primer.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTT3 vector. Library
went through one round of normalization."

ORIGIN

Query Match 71.1%; Score 43.4; DB 7; Length 83;
Best Local Similarity 82.0%; Pred. No. 0.011;
Matches 50; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 AGCTGCCCTCTCTTCTCCCTCACACTACAGCCCTGTTGGGGAGAGGGGGTGGTGC 60
|||||
Db 65 AGCTGTCTTTTTTTCTCTTATCTACTACAGCTTGTGGGGAGAGGGGGTGGTGC 6

QY 61 T 61
Db 5 T 5

RESULT 3

DN374929
LOCUS
DEFINITION DN374929 77 bp mRNA linear EST 07-MAR-2005
LIB38529_027_C11_T7_1 LIB38529 Canis familiaris cDNA clone
LIB38529_027_C11_mRNA sequence.

ACCESSION DN374929
VERSION DN374929.1 GI:60556149
KEYWORDS EST.
SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 77)

AUTHORS Statens N.R.
TITLE Direct Submission (Statens N.R.)

JOURNAL Unpublished (2005)
COMMENT Contact: Nick Statens
Tel: 636 247 6855
Email: nicholas.r.statens@pfizer.com.

FEATURES Location/Qualifiers

source

1. .77
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="LIB38529_027_C11"
/tissue type="heart"
/lab host="DH10B"
/clone lib="LIB38529"
/note="Vector: pSORT1; Site_1: SalI; Site_2: NotI"

ORIGIN

Query Match 45.2%; Score 27.6; DB 9; Length 77;
Best Local Similarity 67.2%; Pred. No. 7.1e+02;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 3 CTGCCCCCTCTTCTCCCTCACACTACAGCCCTGTTGGGGAGAGGGGGTGGTGC 60
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Db 1 CCGCTCTCTCTTCTCCCTCCCCCTCCCGGGGGCGGAGGGCGGGAGGC 58
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RESULT 4

AA731471
LOCUS
DEFINITION AA731471 103 bp mRNA linear EST 05-MAR-1998
n298f08.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1303527 3',
similar to TR:O00146 O00146 P120B4F TRANSCRIPTION FACTOR. i, mRNA
sequence.

ACCESSION AA731471
VERSION AA731471.1 GI:2753627
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 103)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center


```
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 610 row: k column: 23
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 78.
FEATURES
    source
        1..78
            /organism="Sorghum bicolor"
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            /cultivar="ATx623"
            /db_xref="taxon:4558"
            /clone="11173943"
            /clone_lib="Sorghum methylation filtered library (LibID:
            104)"
            /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
            prepared from purified nuclei was randomly sheared,
            end-repaired, size fractionated to enrich for the 0.5 to 5
            kb fraction, ligated into HincII-digested pBCSK(-) vector
            and electroporated into E. coli cells. This is a
            methylation filtered library."
ORIGIN
    Query Match      38.7%; Score 23.6; DB 13; Length 78;
    Best Local Similarity 64.8%; Pred. No. 1.2e+04;
    Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 6 CCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGGGTGGGTG 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 CCCCCCCCCCCCCCCCCCCCCCGCCCTTGGGGGGGGGGGGGGGGGG 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 10
CW189398/c
LOCUS
DEFINITION
    104 610 11173943 148 37098 086 Sorghum methylation filtered library
    (LibID: 104) Sorghum bicolor genomic clone 11173943, genomic survey
    sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
    Sorghum bicolor (sorghum)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
    1 (bases 1 to 78)
    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
    Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
    McWenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
    Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalo, J.A. and
    Martienssen,R.A.
    Sorghum genome sequencing by methylation filtration
    PLoS Biol. 3 (1), e13 (2005)
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 610 row: k column: 23
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 78.
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            /organism="Sorghum bicolor"
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            /clone_lib="Sorghum methylation filtered library (LibID:
            104)"
            /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
            prepared from purified nuclei was randomly sheared,
            end-repaired, size fractionated to enrich for the 0.5 to 5
            kb fraction, ligated into HincII-digested pBCSK(-) vector
            and electroporated into E. coli cells. This is a
            methylation filtered library."
ORIGIN
    Query Match      38.7%; Score 23.6; DB 13; Length 78;
    Best Local Similarity 64.8%; Pred. No. 1.2e+04;
    Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 6 CCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGGGTGGGTG 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 CCCCCCCCCCCCCCCCCCCCCCGCCCTTGGGGGGGGGGGGGGGGGG 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 10
CW189398/c
LOCUS
DEFINITION
    104 610 11173943 148 37098 086 Sorghum methylation filtered library
    (LibID: 104) Sorghum bicolor genomic clone 11173943, genomic survey
    sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
    Sorghum bicolor (sorghum)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
    1 (bases 1 to 78)
    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
    Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
    McWenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
    Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalo, J.A. and
    Martienssen,R.A.
    Sorghum genome sequencing by methylation filtration
    PLoS Biol. 3 (1), e13 (2005)
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 610 row: k column: 23
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 78.
FEATURES
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            /mol_type="genomic DNA"
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            /db_xref="taxon:4558"
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            104)"
            /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
            prepared from purified nuclei was randomly sheared,
            end-repaired, size fractionated to enrich for the 0.5 to 5
            kb fraction, ligated into HincII-digested pBCSK(-) vector
            and electroporated into E. coli cells. This is a
            methylation filtered library."
ORIGIN
    Query Match      38.7%; Score 23.6; DB 13; Length 78;
    Best Local Similarity 64.8%; Pred. No. 1.2e+04;
    Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 6 CCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGGGTGGGTG 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 CCCCCCCCCCCCCCCCCCCCCCGCCCTTGGGGGGGGGGGGGGGGGG 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 11
CW336527/c
LOCUS
DEFINITION
    104 835 11483640 148 36099 082 Sorghum methylation filtered library
    (LibID: 104) Sorghum bicolor genomic clone 11483640, genomic survey
    sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
    Sorghum bicolor (sorghum)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
    1 (bases 1 to 82)
    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
    Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
    McWenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
    Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalo, J.A. and
    Martienssen,R.A.
    Sorghum genome sequencing by methylation filtration
    PLoS Biol. 3 (1), e13 (2005)
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 835 row: o column: 24
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 82.
FEATURES
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            /clone_lib="Sorghum methylation filtered library (LibID:
            104)"
            /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
            prepared from purified nuclei was randomly sheared,
            end-repaired, size fractionated to enrich for the 0.5 to 5
            kb fraction, ligated into HincII-digested pBCSK(-) vector
            and electroporated into E. coli cells. This is a
            methylation filtered library."
ORIGIN
```

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Query Match      38.7%; Score 23.6; DB 13; Length 82;
Best Local Similarity 64.8%; Pred. No. 1.2e+04;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 6 CCCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGAGAGGGGTGGGTG 59
DB 73 CGCGCCCCCCCCCCCCCCCCCCCCCGCGGGGGGGGGGGGGGGGGGG 20

RESULT 12
BH415834/c      91 bp DNA linear GSS 12-DEC-2001
LOCUS 1007045A05.x1 1007 - RescueMu Grid H Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION BH415834
VERSION BH415834.1 GI:17597044
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE Walbot.V.
AUTHORS Zea mays genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1007045 column: 12
Class: transposon-tagged.
FEATURES
source
1..91
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match      38.4%; Score 23.4; DB 11; Length 91;
Best Local Similarity 73.2%; Pred. No. 1.3e+04;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 AGCTGCGCTCTCTTCTCCCTCACACTACAGCCCTGGTG 41
DB 44 ATCGACCTCTCTTCTCCCTTCCCTTCCACACAGCGCCTAGCTAG 4

RESULT 13
BH112776      119 bp mRNA linear EST 11-FEB-2003
LOCUS BP112776 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
DEFINITION ORCS13554 5', mRNA sequence.

```

```

ACCESSION BP112776
VERSION BP112776.1 GI:28315066
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 119)
Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H.,
Takahashi,T., Inai,K., Hirasawa,A., Shiojima,S., Ikawa,H.,
Suzuki,Y., Tsujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.
Characterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray
Mol. Reprod. Dev. 65 (1), 9-18 (2003)
13658628
Contact: Goroh Tsujimoto
Department of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
Tel: 81-3-3149-2476
Fax: 81-3-3149-1252
Email: gtsujimoto@nch.go.jp
This work was performed to collaborate with Developmental Biology
Department, National Institute of Agrobiological Sciences. Address:
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
81-29-838-8633 e-mail: kazuha@affrc.go.jp
This work was funded by Organized Research Combination System
(ORCS) project of Ministry of Education, Culture, Sports, Science
and Technology.
FEATURES
source
1..119
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="ORCS13554"
/tissue_type="mixture of uterus and placenta"
/dev_stage="adult"
/clone_lib="ORCS bovine utero-placenta cDNA"

ORIGIN
Query Match      38.4%; Score 23.4; DB 3; Length 119;
Best Local Similarity 64.7%; Pred. No. 1.4e+04;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 11 CTCTTCTCCCTCACACTACAGCCCTGGTGGGAGAGGGGTGGTGT 61
DB 69 CTCTGCGCACTTCCCTCCAGCCCTGGTGAGCTCCAGTTGGTGGTGT 119

RESULT 14
DN373872      55 bp mRNA linear EST 07-MAR-2005
LOCUS DN373872_002_F03_T7.1 LIB38528 Canis familiaris cDNA clone
DEFINITION LIB38528_002_F03, mRNA sequence.
ACCESSION DN373872
VERSION DN373872.1 GI:60555092
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 55)
Staten,N.R.
Direct Submission (Staten,N.R.)
Unpublished (2005)
Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
FEATURES
source
1..55
/organism="Canis familiaris"

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Search completed: October 14, 2006, 20:24:32
Job time : 2392 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:29:31 ; Search time 2138 Seconds

(without alignments)
1824.505 Million cell updates/sec

Title: US-10-604-926A-1931

Perfect score: 61

Sequence: 1 agctgcctctctctctctcc.....gggagagggggtggtgct 61

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2862434

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_ph.*

4: gb_pl.*

5: gb_pr.*

6: gb_ro.*

7: gb_sts.*

8: gb_sy.*

9: gb_un.*

10: gb_vi.*

11: gb_ov.*

12: gb_hcg.*

13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25.4	41.6	60	2	A62989 Sequence 1
C 2	23.6	38.7	64	2	BD226837 High thro
C 3	23.6	38.7	64	2	BD226837 High thro
C 4	23.2	38.0	100	5	HUMSYNLE08
C 5	22.8	37.4	70	2	AR012477 Sequence
C 6	22.8	37.4	70	2	AR020305 Sequence
C 7	22.8	37.4	70	2	AR109326 Sequence
C 8	22.8	37.4	70	2	AR1368517 Sequence
C 9	22.8	37.4	70	2	I82651 Sequence 92
C 10	22.8	37.4	70	2	AR391709 Sequence
C 11	22.6	37.0	101	4	NEUMTGR7
C 12	22	36.1	66	2	AR072451 Sequence
C 13	22	36.1	66	2	I26562 Sequence 25
C 14	21.4	35.1	100	2	AX989306 Sequence
C 15	21.4	35.1	100	2	AX989307 Sequence
C 16	21.2	34.8	75	2	AR125930 Sequence
C 17	21.2	34.8	75	2	I24297 Sequence 84
C 18	20.8	34.1	100	2	AX989958 Sequence

19	20.8	34.1	100	2	AX989959	AX989959 Sequence
20	20.6	33.8	90	4	AY947208	AY947208 Oryza sat
21	20.6	33.8	91	15	FRA23RRNAB	M85113 Frankia sp.
C 22	20.6	33.8	119	7	G32415	G32415 A009C21 Hum
23	20.4	33.4	52	4	D0358817	D0358817 Viola sp.
24	20.4	33.4	60	2	A62989	A62989 Sequence 1
25	20.4	33.4	81	4	AY947209	AY947209 Oryza sat
C 26	20.2	33.1	112	5	AY878245	AY878245 Homo sapi
27	20	32.8	66	8	SYNINGSAL	J02555 Rat insulin
28	20	32.8	76	2	AR579029	AR579029 Sequence
29	20	32.8	76	2	AX240936	AX240936 Sequence
30	20	32.8	103	5	S7538510	S75404 collagen ty
31	20	32.8	106	2	CQ148149	CQ148149 Sequence
32	20	32.8	106	2	CQ207925	CQ207925 Sequence
C 33	19.6	32.1	51	2	AX411413	AX411413 Sequence
34	19.6	32.1	119	7	BV194603	BV194603 sqm18161
35	19.6	32.1	120	2	AR248658	AR248658 Sequence
36	19.4	31.8	60	2	CQ539983	CQ539983 Sequence
C 37	19.4	31.8	76	2	AR500694	AR500694 Sequence
C 38	19.4	31.8	76	2	AR515976	AR515976 Sequence
39	19.4	31.8	113	14	AF455673	AF455673 Bos tauru
40	19.2	31.5	50	2	AR681052	AR681052 Sequence
C 41	19.2	31.5	103	2	CQ690519	CQ690519 Sequence
C 42	19	31.1	50	2	AR683151	AR683151 Sequence
C 43	19	31.1	57	2	AR000467	AR000467 Sequence
C 44	19	31.1	89	2	CQ107196	CQ107196 Sequence
C 45	19	31.1	93	2	BD040459	BD040459 Sequence

ALIGNMENTS

RESULT 1	A62989	60 bp	DNA	linear	PAT 12-MAR-1998
LOCUS	Sequence 1 from Patent WO9720068.				
DEFINITION	A62989				
ACCESSION	A62989.1	GI:3716861			
VERSION					
KEYWORDS	unidentified				
SOURCE	unclassified sequences.				
ORGANISM	unclassified sequences.				
REFERENCE	1				
AUTHORS	Cerum,H. and Seeger,C.				
TITLE	METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS				
JOURNAL	Patent: WO 9720068-A 1 05-JUN-1997;				
FEATURES	BOEHRINGER MANNHEIM GMBH (DE)				
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	/organism="unidentified"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32644"				

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Best Local Similarity	32.1%;	Pred. NO. 4.8e+02;		
Matches	17;	Conservative 25;	Mismatches 11;	Indels 0; Gaps 0;
Qy	7	CCTCCTCTCTCCCTCAGCTACAGCTGCTGGGGGAGAGGGGTGGTG	59	
Db	60	YY	8	
RESULT 2	BD226837	64 bp	DNA	linear
LOCUS	BD226837			
DEFINITION	High through put method for functionally classifying proteins			
ACCESSION	BD226837			
VERSION	BD226837.1	GI:33036607		
KEYWORDS	JP 2002514571-A/7.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			

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DEFINITION	Sequence 92 from patent US 6376474.				
ACCESSION	AR368517				
VERSION	AR368517.1 GI:34602668				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 70)				
TITLE	Heilig,J.S. and Gold,L. Systematic evolution of ligands by exponential enrichment: tissue SLEX				
JOURNAL	Patent: US 6376474-A 92 23-APR-2002; Gilead Sciences, Inc.; Foster City, CA				
FEATURES	Location/Qualifiers source 1..70 /organism="unknown" /mol_type="genomic DNA"				
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Query Match	37.4%; Score 22.8; DB 2; Length 70;				
Best Local Similarity	66.0%; Pred. No. 4.2e+03;				
Matches	33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;				
<hr/>					
Qy	3 CTGCCCTCCTTCTTCCTCCCTCACACTACAGCCCTGGTGGGGGAGAAGGG 52 				
Db	51 CTACCCTCCTCTGGCGCCAAAGTCACTACTGCCTAGGAGGCTCAACAAG 2 				
<hr/>					
RESULT 9	PAT 10-JUN-1998				
I82651/C					
LOCUS	I82651 Sequence 92 from patent US 5712375. linear				
DEFINITION	Sequence 92 from patent US 5712375.				
ACCESSION	I82651				
VERSION	I82651.1 GI:3210948				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 70)				
TITLE	Jensen,K.B., Chen,H., Morris,K.N., Stephens,A. and Gold,L. Systematic evolution of ligands by exponential enrichment: tissue selex				
JOURNAL	Patent: US 5712375-A 92 27-JAN-1998;				
FEATURES	Location/Qualifiers source 1..70 /organism="unknown" /mol_type="unassigned DNA"				
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Best Local Similarity	66.0%; Pred. No. 4.2e+03;				
Matches	33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;				
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Db	51 CTACCCTCCTCTGGCGCCAAAGTCACTACTGCCTAGGAGGCTCAACAAG 2 				
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RESULT 10	PAT 18-DEC-2003				
AR391709/c					
LOCUS	AR391709 Sequence 92 from patent US 6613526. linear				
DEFINITION	Sequence 92 from patent US 6613526.				
ACCESSION	AR391709				
VERSION	AR391709.1 GI:40115302				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 70)				
TITLE	Heilig,J.S. and Gold,L. Systematic evolution of ligands by exponential enrichment: tissue selex				
JOURNAL	Patent: US 6613526-A 92 02-SEP-2003;				

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Job time : 2141 secs

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:27:16 ; Search time 303 Seconds
(without alignments)
1403.654 Million cell updates/sec

Title: US-10-604-926A-1931
Perfect score: 61
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 5729524

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001as.*
 - 5: Geneseq2001bs.*
 - 6: Geneseq2002as.*
 - 7: Geneseq2002bs.*
 - 8: Geneseq2003as.*
 - 9: Geneseq2003bs.*
 - 10: Geneseq2003cs.*
 - 11: Geneseq2003ds.*
 - 12: Geneseq2004as.*
 - 13: Geneseq2004bs.*
 - 14: Geneseq2005s.*
 - 15: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22.8	37.4	70	2 AAT71418	Aat71418 Glioblast
C 2	21.4	35.1	100	8 ACD69499	Acd69499 E. coli K
C 3	21.4	35.1	100	8 ACD69500	Acd69500 E. coli K
C 4	21.2	34.8	74	14 AED05121	Aed05121 Human IL-
C 5	21.2	34.8	74	14 AED05124	Aed05124 Human IL-
C 6	21.2	34.8	75	2 AAQ98397	Aaq98397 SELEX der
C 7	21.2	34.8	75	4 AAF70810	Aaf70810 Thrombin
C 8	20.8	34.1	100	8 ACD70152	Acd70152 E. coli K
C 9	20.8	34.1	100	8 ACD70151	Acd70151 E. coli K
C 10	20.2	33.1	116	8 ABX41062	Abx41062 Bovine ES
C 11	20	32.8	76	4 AAS23493	Aas23493 C. albica
C 12	20	32.8	106	4 ABA51507	Abas1507 Human bre
C 13	20	32.8	106	4 AAK43614	Aak43614 Human bon
C 14	19.6	32.1	51	6 ABL60621	Ab160621 Nucleotid
C 15	19.6	32.1	51	6 ABK10896	Abk10896 DNA encod
C 16	19.6	32.1	120	10 ABX85557	Abx85557 Corn ear-
C 17	19.4	31.8	57	14 AEB98101	Aeb98101 (SP)10 ge
C 18	19.4	31.8	60	6 ABR36870	Abn36870 Human spl

C 19	19.4	31.8	87	14 AEB98091	Aeb98091 hGH-(SP)1
C 20	19.4	31.8	87	14 AEB98102	Aeb98102 (SP)10 ge
C 21	19.4	31.8	103	14 AEB70564	Aeb70564 Lysyl hyd
C 22	19.4	31.8	116	12 ACH90116	Ach90116 Human gen
C 23	19.2	31.5	37	14 AED05189	Aed05189 Human IL-
C 24	19.2	31.5	50	6 ABZ00490	Abz00490 Human leu
C 25	19.2	31.5	61	3 AAA29504	Aaa29504 Codon alt
C 26	19.2	31.5	66	2 AAQ12354	Aaq12354 Euoplum-
C 27	19.2	31.5	115	4 AAK78349	Aak78349 Human imm
C 28	19	31.1	50	6 ABZ02589	Abz02589 Human leu
C 29	19	31.1	57	2 AAT16237	Aat16237 A. oryzae
C 30	19	31.1	89	4 AAI47369	Aai47369 Probe #16
C 31	19	31.1	93	3 AAC16714	Aac16714 Human sec
C 32	19	31.1	108	12 ADG99660	Adg99660 Kidney di
C 33	19	31.1	118	13 ADR30298	Adr30298 Mouse gen
C 34	19	31.1	120	3 AAC22952	Aac22952 Human sec
C 35	18.8	30.8	40	2 AAQ22624	Aaq22624 Sense oli
C 36	18.8	30.8	60	6 AEN35863	Abn35863 Human spl
C 37	18.8	30.8	65	6 AEN56704	Abn56704 Mouse spl
C 38	18.8	30.8	73	6 AAS20394	Aas20394 Human VL
C 39	18.8	30.8	73	6 AAS20398	Aas20398 Human VL
C 40	18.8	30.8	80	12 ADM95681	Adm95681 Rat antis
C 41	18.8	30.8	84	4 AAI26542	Aai26542 Probe #16
C 42	18.8	30.8	84	4 ABA74773	Abas74773 Human foe
C 43	18.8	30.8	84	4 AAI55297	Aai55297 Probe #23
C 44	18.8	30.8	84	4 ABS49046	Abs49046 Human liv
C 45	18.8	30.8	84	6 ABS22916	Abs22916 Human gen

ALIGNMENTS

RESULT 1
AAT71418/c
ID AAT71418 standard; DNA; 70 BP.

AC AAT71418;

DT 01-AUG-1997 (first entry)

DE Glioblastoma U251 cell line ligand GBI.156.

XX Ligand; glioblastoma; brain; tumour; SELEX; in vivo; imaging;
XX systematic evolution of ligands by exponential enrichment; cancer;
XX drug delivery; cell line; ss.

OS Synthetic.

XX WO9634875-A1.

PD 07-NOV-1996.

PF 01-MAY-1996; 96WO-US006060.

PR 03-MAY-1995; 95US-00433585.

PR 03-MAY-1995; 95US-00434001.

PR 03-MAY-1995; 95US-00434425.

XX (NEXS-) NEXSTAR PHARM INC.

PA (UYRE-) UNIV RES CORP.

XX Jensen KB, Chen H, Morris KN, Stephens A, Gold L;

XX WPI, 1996-506092/50.

PT Identifying nucleic acid ligands for tissues - by contacting candidate
PT mixt. of nucleic acids with tissue and enriching for increased affinity
PT nucleic acids.

PS Claim 22; Page 65; 110pp; English.

CC The present sequence is a single stranded DNA ligand to the human brain


```
Query Match          35.1%; Score 21.4; DB 8; Length 100;
Best Local Similarity 66.0%; Pred. No. 3.2e+03;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 9 TCCTCTTCCCTCCACTACAGCCCTGGTGGGAGAGGGGGTG 55
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 99 TCCTGTCCCTCCACTACCTACCGTGTGTGATGGCGAGCGGCGTG 53

RESULT 4
AED05121
ID AED05121 standard; RNA; 74 BP.
XX
AC AED05121;
XX
DT 01-DEC-2005 (first entry)
XX
DE Human IL-23 binding aptamer, SEQ ID No:91.
XX
KW aptamer; interleukin-23; cytokine; pharmaceutical; diagnostic;
KW autoimmune disease; inflammation; cancer; bone resorption; osteoporosis;
KW insulin dependent diabetes; immunosuppressive; antiinflammatory;
KW cytostatic; osteopathic; antidiabetic; neuroprotective; antirheumatic;
KW antiarthritic; antipsoriatic; dermatological; gastrointestinal-gen.;
KW antiulcer; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..74
FT /*tag= a
FT /mod_base= OTHER
FT /note= "All purines are deoxy and all pyrimidines are 2'-
FT O-methyl"
XX
PN WO2005086835-A2.
XX
PD 22-SEP-2005.
XX
PF 07-MAR-2005; 2005WO-US007666.
XX
PR 05-MAR-2004; 2004US-0550962P.
PR 07-SEP-2004; 2004US-0608046P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Cload ST, Diener JL, Ferguson A, Hamaguchi N, Keene SC;
PI Lagasse HAD, Sawhney P, Thompson K;
XX
WPI; 2005-630794/64.
XX
New aptamer that specifically binds to IL-23 or its variant, useful for
treating, preventing, or ameliorating, e.g. autoimmune disease,
PT inflammatory disease, cancer, bone resorption in osteoporosis, or Type I
PT Diabetes.
XX
Claim 29; SEQ ID NO 91; 305pp; English.
XX
The invention relates to aptamers that specifically bind to interleukin-
23 (IL-23) or interleukin-12 (IL-12), or their variants. The aptamers
CC comprises a nucleotide sequence selected from SEQ ID NOS 13-66, 71-88, 91
CC -96, 103-118, 124-134, 135-159, 162, 164-172, 176-178, 181-196, and 199-
CC 314. Also described are: (1) a pharmaceutical composition comprising an
CC aptamer selected from one cited above, or its salt, and a pharmaceutical
CC carrier or diluent; (2) a method of treating, preventing, or ameliorating
CC a disease mediated by IL-23; (3) a method of treating, preventing, or
CC ameliorating a disease mediated by IL-12; and (4) a diagnostic method
CC comprising contacting an aptamer above with a composition suspected of
CC comprising IL-23 or its variant and detecting the presence or absence of
CC IL-23 or its variant. The aptamers of the invention are useful as in
CC vitro or in vivo diagnostic agents. They are also useful in the
CC treatment, prevention, or amelioration of a disease in vivo. The disease
CC is an autoimmune disease (e.g. multiple sclerosis, rheumatoid arthritis,
```

CC a disease mediated by IL-23; (3) a method of treating, preventing, or
CC ameliorating a disease mediated by IL-12; and (4) a diagnostic method
CC comprising contacting an aptamer above with a composition suspected of
CC comprising IL-23 or its variant and detecting the presence or absence of
CC IL-23 or its variant. The aptamers of the invention are useful as in
CC vitro or in vivo diagnostic agents. They are also useful in the
CC treatment, prevention, or amelioration of a disease in vivo. The disease
CC is an autoimmune disease (e.g. multiple sclerosis, rheumatoid arthritis,
CC psoriasis, systemic lupus erythematosus, or irritable bowel disease),
CC inflammatory disease (e.g. Crohn's Disease or ulcerative colitis), cancer
CC (e.g. colon cancer, lung cancer, or lung metastases), bone resorption in
CC osteoporosis, or Type I Diabetes. This sequence represents an aptamer of
CC the invention.

XX
SQ Sequence 74 BP; 15 A; 13 C; 32 G; 0 T; 14 U; 0 Other;

Query Match 34.8%; Score 21.2; DB 14; Length 74;
Best Local Similarity 64.7%; Pred. No. 3.6e+03;
Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 27 CTACAGCCCTGGTGGGGAGAGAGGGGGTGGTGC 60
|:|||||:|||||:|||||:|||||:|||||:|
Db 19 CUACAGCCCGGGGGGUGGCAUAGGGGUGGAUC 52

RESULT 6

AAQ98397
ID AAQ98397 standard; RNA; 75 BP.

XX
AC AAQ98397;

XX
DT 08-AUG-1996 (first entry)

XX
DE SELEX derived DNA thrombin ligand 30-6.

XX Family 1; family 2; ligand; thrombin;
KW systematic evolution of ligands by exponential enrichment; SELEX;
KW heparin; selection; region of homology; inhibitor; ss.

XX
OS Synthetic.

XX Key Location/Qualifiers
FH misc_feature 1..20
FT /tag= a
FT /note= "Fixed region"
FT misc_feature 21..50
FT /tag= b
FT /note= "Variable region"
FT misc_feature 51..75
FT /tag= c
FT /note= "Fixed region"

XX WO9521853-A1.

XX
PD 17-AUG-1995.

XX
PF 06-FEB-1995; 95WO-US001458.

XX
PR 10-FEB-1994; 94US-00195005.

XX
PR 28-MAR-1994; 94US-00219012.

XX (NEXS-) NEXSTAR PHARM INC.

XX
PI Janjic N, Gold L, Tasset D;

XX
DR WPI; 1995-293073/38.

XX Identification of ligands to basic fibroblast growth factor and thrombin
PT - which can be modified for increased in vivo stability.

XX
PS Claim 39; Page 98; 236pp; English.

XX
XX The sequences given in AAQ98397-405 represent DNA ligands directed to

CC thrombin which were isolated using systematic evolution of ligands by
CC exponential enrichment (SELEX). Two populations of single stranded (ss)
CC DNA molecules with either 30N or 60N variable regions with 5' and 3'
CC fixed regions were synthesised. Thrombin and DNA were incubated in a
CC buffer at 37 deg.C for 5 mins. The thrombin-bound DNA is removed by PCR,
CC filtration. A double stranded product was created and amplified by PCR,
CC and a ssDNA template pool was isolated from this by alkaline
CC denaturation. This ssDNA template pool was used for the following round
CC of SELEX. Individual clones were isolated and the dissociation constants
CC (Kd) were determined. Kd's ranged from 0.4-9.4 nM for the 30N DNA's and
CC from 0.9-2.5 nM for the 60N DNA's. A truncated ligand given in AAQ98404
CC was derived from the high affinity clone 60-18 and has a Kd of 1.9 nM and
CC inhibits clotting

XX
SQ Sequence 75 BP; 14 A; 15 C; 28 G; 18 T; 0 U; 0 Other;

Query Match 34.8%; Score 21.2; DB 2; Length 75;
Best Local Similarity 76.5%; Pred. No. 3.6e+03;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 23 CACACTACAGCCCTGGTGGGGAGAGGGGGTGG 56
|||:|||||:|||||:|||||:|||||:|
Db 15 CATGCTACCCCGTGGTAGGTAGGTGGGGTGG 48

RESULT 7

AAAF70810
ID AAFA70810 standard; DNA; 75 BP.

XX
AC AAFA70810;

XX
DT 20-APR-2001 (first entry)

XX
DE Thrombin high affinity ligand #57.

XX Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;
KW atherosclerosis; angioplasty; stability; ss.

XX
OS Unidentified.

XX
PN US6177557-B1.

XX
PD 23-JAN-2001.

XX
PF 05-AUG-1996; 96US-00687421.

XX
PR 11-JUN-1990; 90US-00536428.

XX
PR 10-JUN-1991; 91US-00714131.

XX
PR 06-NOV-1992; 92US-00973333.

XX
PR 10-FEB-1994; 94US-00195005.

XX
PR 28-MAR-1994; 94US-00219012.

XX (NEXS-) NEXSTAR PHARM INC.

XX
PI Janjic N, Gold L, Tasset D;

XX
DR WPI; 2001-158583/16.

XX Novel nucleic acid ligands to basic fibroblast growth factor that are
PT useful as inhibitors of basic fibroblast growth factors and 2'-amino
PT modified RNA ligands, exhibit increased in vivo stability.

XX
PS Example 19; Col 61-62; 153pp; English.

XX The present invention relates to a purified and isolated non-naturally
CC occurring DNA ligands to basic fibroblast growth factor (bFGF). The
CC ligands are useful as part of gene therapy treatments and for diagnosing
CC pathogenesis of vascular diseases including initiation and progression of
CC atherosclerosis, acute coronary syndromes, vein graft disease and
CC restenosis following coronary angioplasty. The ligands have improved
CC stability in vivo

XX
SQ Sequence 75 BP; 14 A; 15 C; 28 G; 18 T; 0 U; 0 Other;

[illegible]

KW Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer; ss.
 XX Homo sapiens.
 XX OS WO200157271-A2.
 XX PN WO200157271-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000662.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-496933/54.
 XX PT New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 XX Claim 4; SEQ ID NO 10202; 327pp + Sequence Listing; English.
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence data for this
 CC nucleic acid probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 106 BP; 35 A; 24 C; 15 G; 32 T; 0 U; 0 Other;
 Query Match 32.8%; Score 20; DB 4; Length 106;
 Best Local Similarity 65.9%; Pred. No. 8.8e+03;
 Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 OY 6 CCCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAG 49
 DB 29 CCCTCTCTTCTCTCTCTCAATTGGAGATGATGAGATGAAG 72
 RESULT 13
 AAK43614
 ID AAK43614 standard; DNA; 106 BP.
 XX AC AAK43614;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human bone marrow expressed single exon probe SEQ ID NO: 18171.
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX Homo sapiens.
 XX OS WO200157276-A2.
 XX PN WO200157276-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000668.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488900/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX Example 4; SEQ ID NO 18171; 658pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention
 XX SQ Sequence 106 BP; 35 A; 24 C; 15 G; 32 T; 0 U; 0 Other;
 Query Match 32.8%; Score 20; DB 4; Length 106;
 Best Local Similarity 65.9%; Pred. No. 8.8e+03;
 Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 OY 6 CCCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAG 49
 DB 29 CCCTCTCTTCTCTCTCTCAATTGGAGATGATGAGATGAAG 72
 RESULT 14
 ABL60621/c
 ID ABL60621 standard; DNA; 51 BP.
 XX AC ABL60621;
 XX DT 27-AUG-2002 (first entry)
 XX DE Nucleotide fragment from vector pMM106H.
 XX KW Nuclease; tagged protein; protein production; glutathione S transferase;
 KW GST; ds.
 XX OS Synthetic.
 XX WO200227327-A2.
 XX PN WO200227327-A2.
 XX PD 04-APR-2002.
 XX PF 17-AUG-2001; 2001WO-GB003693.
 XX PR 17-AUG-2000; 2000GB-00020357.
 XX PR 14-NOV-2000; 2000US-0247995P.
 XX PA (SENS-) SENSE PROTEOMIC LTD.
 XX PI Blackburn JM, Mulder MA, Samaddar M, Kozlowski R;

```
XX WPI; 2002-471270/50.
DR P-PSDB; ABB08039.
XX
XX Producing proteins having full-length, correctly folded domains and
PT marker moiety-tagged N- or C-terminals, by genetically modifying cDNA to
PT encode individual protein having marker moiety fused to N- or C-terminus.
XX
XX Example; Fig 1a; 47pp; English.
PS
XX The invention relates to producing full-length proteins incorporating
XX alpha-S-DNTPs into DNA (I) encoding protein, protecting ends of
CC (I) from nuclease digestion, generating (I) in which set of nested
CC deletions are generated and 5' or 3' untranslated region (UTR) of open
CC reading frame (ORF) are removed, by nuclease digestion, cloning fragments
CC into vector having coding sequence for 5'/3' marker moiety, and
CC expressing proteins. An array comprising proteins prepared by the above
CC method is useful for screening one or more compounds for biological
CC activity; one or more proteins for specific protein-protein interactions
CC or protein-nucleic acid interactions. The array is useful in the rapid
CC screening of a protein, compound or nucleic acid, and also for screening
CC for molecules (preferably, antibodies) which recognize each protein in
CC the array. It is also useful for generating an antibody array. The tagged
CC proteins produced by the methods are useful for analysis of interaction
CC between expressed protein and other proteins, immobilisation on an
CC affinity column/substrate for example to allow the purification by
CC affinity chromatography of, interacting proteins, DNA or chemical
CC compounds; in the immobilization by affinity purification for
CC microarray for identifying DNA binding proteins; or for elucidating the
CC identity of proteins in the proteome, where mass spectrometric analysis
CC of expressed protein components of source library or start material
CC modified by the methods, are performed. The antibody arrays produced
CC using (I) are useful for screening of protein function or abundance. The
CC present sequence represents nucleotide fragment from vector pMW106H
XX
SQ Sequence 51 BP; 19 A; 19 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 32.1%; Score 19.6; DB 6; Length 51;
Best Local Similarity 73.5%; Pred. No. 1.1e+04;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 28 TACAGCCCTGGTGGGAGAGAGGGGGTGGTGCT 61
DB 46 TAGAGCCCTAGTGGTGGTGGTGGTGGTGGT 13
RESULT 15
ID ABK10896/c
XX ABK10896 standard; DNA; 51 BP.
AC ABK10896;
XX
XX 21-MAY-2002 (first entry)
XX
XX DNA encoding polyasparagine, hexahistidine fusion peptide (Asn-His tag).
XX
XX Jellyfish; protein array; marker group tag; rapid screening;
KW fusion peptide; da.
XX
XX Aequorea victoria.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH 4..51
FT CDS /tag= a
FT /partial
FT /product= "Polyasparagine hexahistidine fusion peptide"
FT /transl_except= (Pos:37..39, aa:Glu)
FT /note= "This sequence lacks both a start and stop codon"
FT 4..36
FT misc_feature /tag= b
FT
```

```
FT misc_feature /note= "Encodes Asn-His tag"
FT 40..52
FT /*tag= C
FT /note= "Encodes jellyfish green fluorescent protein
XX (GFP)"
XX
XX WO200157198-A2.
XX
XX 09-AUG-2001.
XX
XX 31-JAN-2001; 2001WO-GB000395.
XX
XX 31-JAN-2000; 2000GB-00002215.
XX
XX 12-APR-2000; 2000US-0196490P.
XX
XX 11-AUG-2000; 2000GB-00019888.
XX
XX (SENS-) SENSE PROTEOMIC LTD.
XX
XX Blackburn JM, Sutherland JD, Samaddar M, Mulder MA, Kozlowski RZ;
XX
XX WPI; 2002-226206/28.
XX
XX P-PSDB; AAU77202.
XX
XX Method for generating a protein array for the rapid screening of a
XX compound, protein or nucleic acid, comprises cloning and expressing
XX protein(s) as full length protein(s), which are tagged with a marker
XX group at either the N- or C-terminal.
XX
XX Example 1; Fig 1a; 47pp; English.
XX
XX The present invention relates to a new method of generating a protein
XX array. The method of the invention involves cloning and expressing one or
XX more proteins as full length proteins, which are each tagged at either
XX the N- or C-terminal with a marker group. The method is useful for
XX providing or generating an array. The array is useful in the rapid
XX screening of a compound, protein or nucleic acid, and in screening for
XX molecules that recognise each protein in the array, where the molecules
XX are preferably antibodies. The present nucleic acid sequence encodes the
XX polyasparagine hexahistidine fusion peptide of the invention. The peptide
XX contains a histidine tag followed by an amber stop codon which is then
XX followed by the gene encoding the green fluorescent protein (GFP) of the
XX jellyfish Aequorea victoria
XX
XX Sequence 51 BP; 19 A; 19 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 32.1%; Score 19.6; DB 6; Length 51;
Best Local Similarity 73.5%; Pred. No. 1.1e+04;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 28 TACAGCCCTGGTGGGAGAGAGGGGGTGGTGCT 61
DB 46 TAGAGCCCTAGTGGTGGTGGTGGTGGTGGT 13
Search completed: October 14, 2006, 19:32:29
Job time : 307 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:32:46 ; Search time 100 Seconds

(without alignments)
1141.376 Million cell updates/sec

Title: US-10-604-926A-1931

Perfect score: 61

Sequence: 1 agctgcctctctctctcc.....gggagagggtgggtgct 61

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1580294

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22.8	37.4	70	2 US-08-434-001-92	Sequence 92, Appl
C 2	22.8	37.4	70	2 US-08-433-585-92	Sequence 92, Appl
C 3	22.8	37.4	70	2 US-08-434-425-92	Sequence 92, Appl
C 4	22.8	37.4	70	2 US-08-437-667-92	Sequence 92, Appl
C 5	22.8	37.4	70	3 US-08-906-955-92	Sequence 92, Appl
C 6	22.8	37.4	70	3 US-08-945-909-92	Sequence 92, Appl
C 7	22.8	37.4	70	3 US-09-396-002A-92	Sequence 92, Appl
C 8	22.8	37.4	70	3 US-10-077-319-92	Sequence 92, Appl
C 9	22.8	37.4	70	7 PCT-US96-06060-92	Sequence 92, Appl
C 10	22	36.1	66	2 US-07-977-284A-254	Sequence 254, App
C 11	22	36.1	66	2 US-08-256-426B-254	Sequence 254, App
C 12	21.2	34.8	75	3 US-08-219-012-84	Sequence 84, Appl
C 13	21.2	34.8	75	3 US-08-687-421-272	Sequence 272, App
C 14	20	32.8	76	3 US-09-792-024-174	Sequence 174, App
C 15	19.6	32.1	120	3 US-09-313-294A-4017	Sequence 4017, Ap
C 16	19.4	31.8	76	3 US-09-270-767-5654	Sequence 5654, Ap
C 17	19.4	31.8	76	3 US-09-270-767-20936	Sequence 20936, A
C 18	19.2	31.5	50	3 US-10-131-827-481	Sequence 481, App
C 19	19.2	31.5	50	3 US-10-131-831-481	Sequence 481, App
C 20	19	31.1	50	3 US-10-131-827-2580	Sequence 2580, Ap
C 21	19	31.1	50	5 US-10-131-831-2580	Sequence 2580, Ap
C 22	19	31.1	57	2 US-08-596-985-4	Sequence 4, Appl
C 23	19	31.1	93	3 US-09-513-999C-20789	Sequence 20789, A

24	19	31.1	120	3 US-09-513-999C-27027	Sequence 27027, A
25	18.8	30.8	37	3 US-09-025-769B-112	Sequence 112, App
26	18.8	30.8	37	3 US-09-490-070A-112	Sequence 112, App
27	18.8	30.8	37	3 US-09-490-153-112	Sequence 112, App
28	18.8	30.8	37	3 US-09-490-324-112	Sequence 112, App
C 29	18.8	30.8	94	3 US-09-513-999C-33460	Sequence 33460, A
C 30	18.8	30.8	97	2 US-08-447-172A-23	Sequence 23, Appl
C 31	18.6	30.5	41	3 US-09-376-097-21	Sequence 21, Appl
C 32	18.6	30.5	73	2 US-08-318-193-32	Sequence 32, Appl
C 33	18.6	30.5	81	2 US-08-318-193-31	Sequence 31, Appl
34	18.6	30.5	81	10 5200327-12	Patent No. 5200327
35	18.6	30.5	104	3 US-09-404-879A-322	Sequence 322, App
36	18.6	30.5	104	3 US-09-667-857-322	Sequence 322, App
37	18.6	30.5	104	3 US-10-198-053-322	Sequence 322, App
38	18.6	30.5	104	3 US-09-827-271-322	Sequence 322, App
C 39	18.6	30.5	116	3 US-08-787-739-96	Sequence 96, Appl
C 40	18.6	30.5	116	3 US-09-178-115-96	Sequence 96, Appl
C 41	18.6	30.5	116	3 US-09-177-776-96	Sequence 96, Appl
42	18.4	30.2	30	2 US-08-219-012-31	Sequence 31, Appl
43	18.4	30.2	30	3 US-08-687-421-219	Sequence 219, App
44	18.4	30.2	88	3 US-08-464-700-9	Sequence 9, Appl
C 45	18.4	30.2	90	3 US-08-464-700-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-434-001-92/c
; Sequence 92, Application US/08434001
; Patent No. 5712375
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
; TITLE OF INVENTION: SELEX
; NUMBER OF SEQUENCES: 235
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,001
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 70 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-434-001-92

Query Match 37.4%; Score 22.8; DB 2; Length 70;

Best Local Similarity 66.0%; Pred. No. 1.8e+02;

Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CTGCCCTCTCTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGG 52

Db 51 CTACCCCTCTCTGGCCCCAAGTCACTACTGCTAGGAGGCTCACACAGG 2

RESULT 2

US-08-433-585-92/c

; Sequence 92, Application US/08433585

; Patent No. 5763566

; GENERAL INFORMATION:

; APPLICANT: JENSEN, KIRK

; APPLICANT: CHEN, HANG

; APPLICANT: MORRIS, KEVIN

; APPLICANT: STEPHENS, ANDREW

; APPLICANT: GOLD, LARRY

; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY

; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE

; NUMBER OF SEQUENCES: 235

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB

; COMPUTER: IBM pc compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,585

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/536,428

; FILING DATE: 11-JUNE-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/964,624

; FILING DATE: 21-OCTOBER-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX30.4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 70 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-433-585-92

Query Match

Best Local Similarity 37.4%; Score 22.8; DB 2; Length 70;

; Sequence 92, Application US/08437667

Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CTGCCCTCTCTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGG 52

Db 51 CTACCCCTCTCTGGCCCCAAGTCACTACTGCTAGGAGGCTCACACAGG 2

RESULT 3

US-08-434-425-92/c

; Sequence 92, Application US/08434425

; Patent No. 5789157

; GENERAL INFORMATION:

; APPLICANT: JENSEN, KIRK

; APPLICANT: CHEN, HANG

; APPLICANT: MOREIS, KEVIN

; APPLICANT: STEPHENS, ANDREW

; APPLICANT: GOLD, LARRY

; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY

; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE

; NUMBER OF SEQUENCES: 235

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB

; COMPUTER: IBM pc compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/434,425

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/536,428

; FILING DATE: 11-JUNE-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/964,624

; FILING DATE: 21-OCTOBER-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX30.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 70 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-434-425-92

Query Match

Best Local Similarity 37.4%; Score 22.8; DB 2; Length 70;

; Sequence 92, Application US/08437667

Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CTGCCCTCTCTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGG 52

Db 51 CTACCCCTCTCTGGCCCCAAGTCACTACTGCTAGGAGGCTCACACAGG 2

RESULT 4

US-08-437-667-92/c

; Sequence 92, Application US/08437667

Patent No. 5864026
GENERAL INFORMATION:
APPLICANT: JENSEN, KIRK
APPLICANT: CHEN, HANG
APPLICANT: MORRIS, KEVIN
APPLICANT: STEPHENS, ANDREW
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
TITLE OF INVENTION: SELEX
NUMBER OF SEQUENCES: 235
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/437,667
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX30.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-437-667-92

Query Match 37.4%; Score 22.8; DB 2; Length 70;
Best Local Similarity 66.0%; Pred. No. 1.8e+02;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 3 CTGCCCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGGAGAGGGG 52
DB 51 CTACCTCTCTGGCCCAAGTCACTACTGCTAGGAGGCTCACACAGG 2

RESULT 5
US-08-906-955-92/c
Sequence 92, Application US/08906955
Patent No. 6013443
GENERAL INFORMATION:
APPLICANT: HEILIG, JOSEPH S.
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
TITLE OF INVENTION: SELEX
NUMBER OF SEQUENCES: 240
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,955
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,001
FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX30-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-906-955-92

Query Match 37.4%; Score 22.8; DB 3; Length 70;
Best Local Similarity 66.0%; Pred. No. 1.8e+02;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 3 CTGCCCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGGAGAGGGG 52
DB 51 CTACCTCTCTGGCCCAAGTCACTACTGCTAGGAGGCTCACACAGG 2

RESULT 6
US-08-945-909-92/c
Sequence 92, Application US/08945909
Patent No. 6114120
GENERAL INFORMATION:
APPLICANT: JENSEN, KIRK
APPLICANT: CHEN, HANG
APPLICANT: MORRIS, KEVIN
APPLICANT: STEPHENS, ANDREW
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS
TITLE OF INVENTION: ENRICHMENT: TISSUE SELEX
NUMBER OF SEQUENCES: 240
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,909
FILING DATE:
CLASSIFICATION: 435

RESULT 7
US-09-396-002A-92/c
; Sequence 92, Application US/09396002A
; Patent No. 6376474
; GENERAL INFORMATION:
; APPLICANT: HEILIG, JOSEPH S.
; GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; EXPONENTIAL ENRICHMENT: TISSUE SELEX
; NUMBER OF SEQUENCES: 240
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 1745 Shea Center Drive, Suite 330
; CITY: Highlands Ranch
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80129
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/396,002A
; FILING DATE: 14-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; APPLICATION NUMBER: 08/434,001
; FILING DATE: 05-MAY-1995
; APPLICATION NUMBER: 08/906,955
; FILING DATE: 05-AUGUST-1997
; ATTORNEY/AGENT INFORMATION:

```

1  GOLD, LARRY
2  TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
3  NUMBER OF SEQUENCES: 240
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Swanson & Bratschun, L.L.C.
6  STREET: 1745 Shea Center Drive, Suite 330
7  CITY: Highlands Ranch
8  STATE: Colorado
9  COUNTRY: USA
10 ZIP: 80129
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
13 COMPUTER: IBM pc compatible
14 OPERATING SYSTEM: MS-DOS
15 SOFTWARE: WordPerfect 8.0
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/10/077,319
18 FILING DATE: 14-Feb-2002
19 CLASSIFICATION: <Unknown>
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 09/396,002
22 FILING DATE: 14-Sep-1999
23 APPLICATION NUMBER: 07/714,131
24 FILING DATE: 10-JUNE-1991
25 APPLICATION NUMBER: 08/434,001
26 FILING DATE: 05-MAY-1995
27 APPLICATION NUMBER: 08/906,955
28 FILING DATE: 05-AUGUST-1997
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Barry J. Swanson
31 REGISTRATION NUMBER: 33,215
32 REFERENCE/DOCKET NUMBER: NEX30-5/D
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (303) 268-0066
35 TELEFAX: (303) 268-0065
36 INFORMATION FOR SEQ ID NO: 92:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 70 base pairs
39 TYPE: nucleic acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 SEQUENCE DESCRIPTION: SEQ ID NO: 92:

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```
; Sequence 254, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Frockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; NUMBER OF SEQUENCES: 293
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256.426B
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10964
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,284
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-256-426B-254

Query Match 36.1%; Score 22; DB 2; Length 66;
Best Local Similarity 63.0%; Pred. No. 3.3e+02;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 6 CCCTCTCTTCTCCCTCACACTACAGCCCTGTGGGGGAGAGGGGGTGGTG 59
Db 55 CTCCTCTTCTTCTCCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2

RESULT 12
US-08-219-012-84
; Sequence 84, Application US/08219012
; Patent No. 5543293
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Diane Tasset
; TITLE OF INVENTION: Ligands of Thrombin
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, Suite #
; CITY: Denver

; Sequence 254, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Frockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; NUMBER OF SEQUENCES: 293
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,012
; FILING DATE: 08-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/195,005
; FILING DATE: 10-FEBRUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 22-APRIL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/219,012
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; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,012
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: none
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-219-012-84

Query Match 34.8%; Score 21.2; DB 2; Length 75;
Best Local Similarity 76.5%; Pred. No. 6.2e+02;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 23 CACACTACAGCCCTGTGGGGGAGAGGGGGTGG 56
Db 15 CATGCTACACCCGTGGTAGGGTAGGTGGGGTGG 48

RESULT 13
US-08-687-421-272
; Sequence 272, Application US/08687421
; Patent No. 6177557
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Janjic, Nebojsa
; APPLICANT: Tasset, Diane
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 445
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,421
; FILING DATE: 08-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/195,005
; FILING DATE: 10-FEBRUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 22-APRIL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/219,012
```

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; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4017
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700347543HI
US-09-313-294A-4017

Query Match 32.1%; Score 19.6; DB 3; Length 120;
Best Local Similarity 73.5%; Pred. No. 2.2e+03;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0

Qy 3 CTGCCCTCCTCTTCTCCGCTCACACTACAGCCCT 36
Dd 49 CTGGCTCCTCTTCTCCGCTCAGGCTCCCTCCT 82

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Search completed: October 14, 2006, 19:34:35
Job time : 102 secs

Qy 3 CTGCCCTCCTCTTCTCCCTTCACACTACAGCCCT 36
|||||
Db 49 CTGCGGTCTCTCTTTCCCTTCAGCCTCCCCCTCCT 82
|||||

FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 272:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-687-421-272

Query Match	34.8%	Score 21.2;	DB 3;	Length 75;
Best Local Similarity	76.5%	Pred. No. 6.2e+02;		
Matches	26;	Conservative	0;	Mismatches 8;
				Indels 0;
				Gaps 0;

Qy	23	CACACTACAGCCCTGGTGGGGGAGAAAGGGGTGG	56
Dβ	15	CATGCTACACCCGCTGGTAGGGTAGGATGGGGTGG	48

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RESULT 14
US-09-792-024-174
; Sequence 174, Application US/09792024
; Patent No. 6783985
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE REFERENCE: Targets Discovery
; CURRENT APPLICATION NUMBER: US/09/792,024
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 490
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA primer
US-09-792-024-174

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Query Match	32.8%	Score 20;	DB 3;	Length 76;
Best Local Similarity	61.5%	Pred. No. 1.5e+03;		
Matches	32;	Conservative	0;	Mismatches 20;
				Indels 0;
				Gaps 0;

Qy 3 CTGGCCTCGCTTCTCTCCCTCACA CTACAGCCCTGGTGGGGGGAAGAGGGGGT 54

Db 23 CTCTCTCTCTCGTCTCCGCCCTCA CCAACAGCCCGCTCTAGAACTAGTGGAT 74

RESULT 15
US-09-313-294A-4017
; Sequence 4017, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalqudi, Raqhunath V.

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Result No.	Score	Query Match	Length	DB	ID	Description
1	61	100.0	61	11	US-10-310-914A-14543	Sequence 14543, A
2	25	41.0	25	15	US-11-131-849-23506	Sequence 23506, A
3	24.2	39.7	61	11	US-10-310-914A-14543	Sequence 14543, A
4	23.6	38.7	64	6	US-10-057-940-7	Sequence 7, Appl
5	23.6	38.7	64	6	US-10-057-940-7	Sequence 7, Appl
6	23	37.7	23	11	US-10-310-914A-148966	Sequence 148966, A
7	23	37.7	23	11	US-10-310-914A-148976	Sequence 148976, A
8	23	37.7	23	11	US-10-310-914A-1065883	Sequence 1065883, A
9	23	37.7	23	11	US-10-310-914A-1065889	Sequence 1065889, A
10	22.8	37.4	70	6	US-10-077-319-92	Sequence 92, Appl
11	22	36.1	22	11	US-10-310-914A-148933	Sequence 148933, A
12	22	36.1	22	11	US-10-310-914A-148939	Sequence 148939, A
13	22	36.1	22	11	US-10-310-914A-1065861	Sequence 1065861, A
14	22	36.1	22	11	US-10-310-914A-1065867	Sequence 1065867, A
15	22	36.1	22	11	US-10-310-914A-148934	Sequence 148934, A
16	21.2	34.8	61	11	US-10-310-914A-3094	Sequence 3094, A
17	21.2	34.8	85	11	US-10-310-914A-16745	Sequence 16745, A

; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 23506
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-23506

Query Match 41.0%; Score 25; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 CTCACACTACAGCCCTGGTGGGGA 45
Db 1 CTCACACTACAGCCCTGGTGGGGA 25

RESULT 3
US-10-310-914A-14543/c
; Sequence 14543, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14543
; LENGTH: 61
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-14543

Query Match 39.7%; Score 24.2; DB 11; Length 61;
Best Local Similarity 62.3%; Pred. No. 1.5e+02;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 AGCTGCCCTCTCTCTCCCTCACAACACTACAGCCCTGGTGGGGGAGAGGGGTGGTGC 60
Db 61 AGCACCCACCCCTCTCTCCCAACACAGGCTGTAGTGTAGGGGAGAGAGGAGGCGAGC 2
Qy 61 T 61
Db 1 T 1

RESULT 4
US-10-057-940-7
; Sequence 7, Application US/10057940
; Publication No. US20020168686A1
; GENERAL INFORMATION:
; APPLICANT: Pantoliano, Michael W.
; APPLICANT: Carver, Jr., Theodore, E.
; TITLE OF INVENTION: High Throughput Method for Functionally Classifying Proteins
; FILE REFERENCE: 1503.0310002/JAG/JSO
; CURRENT APPLICATION NUMBER: US/10/057,940
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/190,128
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/065,129
; PRIOR FILING DATE: 1997-11-12

; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 64
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: GC-rich tract
US-10-057-940-7

Query Match 38.7%; Score 23.6; DB 6; Length 64;
Best Local Similarity 64.8%; Pred. No. 2.4e+02;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 6 CCCTCCTCTCTCCCTCACAACACTACAGCCCTGGTGGGGGAGAGGGGTGGGTG 59
Db 2 CCCGGGGGGGGGG 55

RESULT 5
US-10-057-940-7/c
; Sequence 7, Application US/10057940
; Publication No. US20020168686A1
; GENERAL INFORMATION:
; APPLICANT: Pantoliano, Michael W.
; APPLICANT: Carver, Jr., Theodore, E.
; TITLE OF INVENTION: High Throughput Method for Functionally Classifying Proteins
; FILE REFERENCE: 1503.0310002/JAG/JSO
; CURRENT APPLICATION NUMBER: US/10/057,940
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/190,128
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/065,129
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 64
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: GC-rich tract
US-10-057-940-7

Query Match 38.7%; Score 23.6; DB 6; Length 64;
Best Local Similarity 64.8%; Pred. No. 2.4e+02;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 6 CCCTCCTCTCTCCCTCACAACACTACAGCCCTGGTGGGGGAGAGGGGTGGGTG 59
Db 63 CCCGGGGGGGGGGGG 10

RESULT 6
US-10-310-914A-148966/c
; Sequence 148966, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148966
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-148966

Query Match 37.7%; Score 23; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GTGGGGGAGAGGGGTGGGTGC 60
Db 23 GTGGGGGAGAGGGGTGGGTGC 1

RESULT 7

US-10-310-914A-148976/c
; Sequence 148976, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148976
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148976
Query Match 37.7%; Score 23; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCTCCTCTTCTCCCTCACACTA 29
Db 23 CCTCCTCTTCTCCCTCACACTA 1

RESULT 8

US-10-310-914A-1065883/c
; Sequence 1065883, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065883
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065883
Query Match 37.7%; Score 23; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GTGGGGGAGAGGGGTGGGTGC 60
Db 23 GTGGGGGAGAGGGGTGGGTGC 1

RESULT 9

US-10-310-914A-1065889/c
; Sequence 1065889, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065889
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065889

Query Match 37.7%; Score 23; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCTCCTCTTCTCCCTCACACTA 29
Db 23 CCTCCTCTTCTCCCTCACACTA 1

RESULT 10

US-10-077-319-92/c
; Sequence 92, Application US/10077319
; Publication No. US20030027781A1
; GENERAL INFORMATION:
; APPLICANT: HEILIG, JOSEPH S.
; GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; EXPONENTIAL ENRICHMENT: TISSUE SELEX
; NUMBER OF SEQUENCES: 240
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 1745 Shea Center Drive, Suite 330
; CITY: Highlands Ranch
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80129
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/077,319
; FILING DATE: 14-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/396,002
; FILING DATE: 14-Sep-1999
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; APPLICATION NUMBER: 08/434,001
; FILING DATE: 05-MAY-1995
; APPLICATION NUMBER: 08/906,955
; FILING DATE: 05-AUGUST-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30-5/D
; TELEPHONE: (303) 268-0065
; TELEFAX: (303) 268-0065
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-10-077-319-92

Query Match      37.4%; Score 22.8; DB 6; Length 70;
Best Local Similarity 66.0%; Pred. No. 4.5e+02;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy  3 CTGCCCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGG 52
    |||||
Db  51 CTACCCCTCTCTGGCCCAAGTCACTACTGCTAGGAGGCTCAACAACAG 2

RESULT 11
US-10-310-914A-148933/c
; Sequence 148933, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148933
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148933

Query Match      36.1%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  34 CCTGTGGGGGAGAGGGGGTG 55
    |||||
Db  22 CCTGTGGGGGAGAGGGGGTG 1

RESULT 12
US-10-310-914A-148939/c
; Sequence 148939, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148939
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148939

Query Match      36.1%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  36 TGGTGGGGAGAGGGGGTGGG 57
    |||||
Db  22 TGGTGGGGAGAGGGGGTGGG 1

RESULT 13
US-10-310-914A-1065861/c
; Sequence 1065861, Application US/10310914A
```

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065861
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065861

Query Match      36.1%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  34 CCTGTGGGGGAGAGGGGGTG 55
    |||||
Db  22 CCTGTGGGGGAGAGGGGGTG 1

RESULT 14
US-10-310-914A-1065867/c
; Sequence 1065867, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065867
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065867

Query Match      36.1%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  36 TGGTGGGGAGAGGGGGTGGG 57
    |||||
Db  22 TGGTGGGGAGAGGGGGTGGG 1

RESULT 15
US-10-310-914A-148934/c
; Sequence 148934, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148934
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
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Search completed: October 14, 2006, 20:23:46
Job time : 848 secs

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RESULT 2
US-11-234-676-94
; Sequence 94, Application US/11234676
; Publication No. US20060193821A1
; GENERAL INFORMATION:
; APPLICANT: Cload, Sharon T.
; APPLICANT: Diener, John L.
; APPLICANT: Ferguson, Alicia
; APPLICANT: Hamaguchi, Nobuko
; APPLICANT: Keene, Sara C.
; APPLICANT: Lagasse, H.A. Daniel
; APPLICANT: Sawhney, Poja
; APPLICANT: Thompson, Kristin
; TITLE OF INVENTION: Aptamers to the Human IL-12 Cytokine Family and Their Use as
; TITLE OF INVENTION: Autoimmune Disease Therapeutics
; FILE REFERENCE: 23239-578 CIP
; CURRENT APPLICATION NUMBER: US/11/234,676
; CURRENT FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 11/075,649
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/550,962
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/608,046
; PRIOR FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 323
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
; LENGTH: 74
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: synthetic aptamer
; NAME/KEY: modified base
; LOCATION: (1)..(74)
; OTHER INFORMATION: all purines (A and G) are deoxy, all pyrimidines (C and U) are
; OTHER INFORMATION: 2'-O-methyl
US-11-234-676-94

Query Match 34.8%; Score 21.2; DB 7; Length 74;
Best Local Similarity 64.7%; Pred. No. 5.4e+02;
Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 27 CTACAGCCCTGTGGGGAGAGAGGGGGTGGTGC 60
|:|||||:|||||:|||||:|||||:|||||:
Db 19 CUACAGCGCGGUGGUGGCAUAGGUGGUAUGC 52

RESULT 3
US-11-036-257-48
; Sequence 48, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 48

Query Match 34.8%; Score 21.2; DB 7; Length 74;
Best Local Similarity 64.7%; Pred. No. 5.4e+02;
Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 27 CTACAGCCCTGTGGGGAGAGAGGGGGTGGTGC 60
|:|||||:|||||:|||||:|||||:|||||:
Db 19 CUACAGCGCGGUGGUGGCAUAGGUGGUAUGC 52

RESULT 3
US-11-036-257-48
; Sequence 48, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 48
```

```
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-036-257-48

Query Match 31.8%; Score 19.4; DB 9; Length 57;
Best Local Similarity 79.3%; Pred. No. 2e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 28 TACAGCCCTGTGGGGGAGAGAGGGGGTGG 56
|:|||||:|||||:|||||:|||||:|||||:
Db 8 TACAGCTATGGCTGGGAGAGAGGGGATGG 36

RESULT 4
US-11-036-257-39/c
; Sequence 39, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 39
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-036-257-39

Query Match 31.8%; Score 19.4; DB 9; Length 87;
Best Local Similarity 79.3%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 28 TACAGCCCTGTGGGGGAGAGAGGGGGTGG 56
|:|||||:|||||:|||||:|||||:|||||:
Db 80 TACAGCTATGGCTGGGAGAGAGGGGATGG 52

RESULT 5
US-11-036-257-49/c
; Sequence 49, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; SEQ ID NO 49
```

; APPLICANT: Cload, Sharon T.

; Sequence 96, Application US/11356568A
 ; Publication No. US20060188981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harris, Adrian
 ; APPLICANT: Ratcliffe, Peter
 ; TITLE OF INVENTION: MN Gene and Protein
 ; FILE REFERENCE: D-0021.5C-3
 ; CURRENT APPLICATION NUMBER: US/11/356,568A
 ; CURRENT FILING DATE: 2006-02-17
 ; PRIOR APPLICATION NUMBER: 10/319,003
 ; PRIOR FILING DATE: 2002-12-13
 ; PRIOR APPLICATION NUMBER: 60/341,036
 ; PRIOR FILING DATE: 2001-12-13
 ; NUMBER OF SEQ ID NOS: 154
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 96
 ; LENGTH: 116
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-11-356-568A-96

Query Match 30.5%; Score 18.6; DB 7; Length 116;
 Best Local Similarity 57.9%; Pred. No. 4.6e+03;
 Matches 33; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 5 GCCCTCTCTCTCCCTCACACTACAGCCCTGTGGGGGAGAGGGGGTGGTGT 61
 Db 57 GCCCTGTGCTCTCTCTCCCCCATACCAAGCTAGGATGGGGGTGGAGTGGGGGCGAGGT 1

RESULT 10

US-11-292-078-10537
 ; Sequence 10537, Application US/11292078
 ; Publication No. US20060195941A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Deikman, Jill
 ; APPLICANT: Feng, Paul C.C.
 ; APPLICANT: Fincher, Karen L.
 ; APPLICANT: Ziegler, Todd E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 16517.346 - 38-21(52274)C
 ; CURRENT APPLICATION NUMBER: US/11/292,078
 ; CURRENT FILING DATE: 2005-12-02
 ; PRIOR APPLICATION NUMBER: US 10/021,323
 ; PRIOR FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: US 60/255,619
 ; PRIOR FILING DATE: 2000-12-14
 ; NUMBER OF SEQ ID NOS: 17880
 ; SEQ ID NO 10537
 ; LENGTH: 73
 ; TYPE: DNA
 ; ORGANISM: Gossypium hirsutum
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3828-028-Q6-N6-B4
 US-11-292-078-10537

Query Match 29.8%; Score 18.2; DB 7; Length 73;
 Best Local Similarity 61.7%; Pred. No. 5.5e+03;
 Matches 29; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 8 CTCCTCTCTCTCCCTCACACTACAGCCCTGTGGGGGAGAGGGGGT 54
 Db 8 CCCCCCTTTTCCCCCCCCCCCCCCCCCTTTTGGGGGGGGGTGT 54

RESULT 11

US-11-266-748A-76054/C
 ; Sequence 76054, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick

; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266,748A
 ; CURRENT FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: Patent In version 3.3
 ; SEQ ID NO 76054
 ; LENGTH: 120
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-266-748A-76054

Query Match 29.5%; Score 18; DB 8; Length 120;
 Best Local Similarity 80.8%; Pred. No. 7.3e+03;
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 32 GCCCTGTGGGGGAGAGGGGGTGGG 57
 Db 26 GCTAGGGTAGGGGAGATGGGGTGGG 1

RESULT 12

US-11-266-748A-109214/C
 ; Sequence 109214, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266,748A
 ; CURRENT FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: Patent In version 3.3
 ; SEQ ID NO 109214
 ; LENGTH: 120
 ; TYPE: DNA

```

; ORGANISM: Homo Sapiens
US-11-266-748A-109214

Query Match      29.5%; Score 18; DB 8; Length 120;
Best Local Similarity 80.8%; Pred. No. 7.3e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 32 GCCTGTGGGAGGAAGGGGTGGG 57
   ||| ||||| ||||| |||||
DB 26 GCTAGGGTAGGGAGATGGGGTGGG 1

RESULT 13
US-11-266-748A-128865
; Sequence 128865, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 128865
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-128865

Query Match      29.5%; Score 18; DB 8; Length 120;
Best Local Similarity 80.8%; Pred. No. 7.3e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 32 GCCTGTGGGAGGAAGGGGTGGG 57
   ||| ||||| ||||| |||||
DB 95 GCTAGGGTAGGGAGATGGGGTGGG 120

RESULT 14
US-11-244-330A-2130
; Sequence 2130, Application US/11244330A
; Publication No. US20060195932A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2005-10-06
; SEARCH completed: October 14, 2005, 19:38:23
Job time : 121 secs

; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 2130
; LENGTH: 101
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700100849H1
US-11-244-330A-2130

Query Match      28.9%; Score 17.6; DB 7; Length 101;
Best Local Similarity 65.0%; Pred. No. 9.5e+03;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 TGCCTCCTCTTCCTCCCTCACACTACAGCCCTGGTGGG 43
   ||| ||||| ||| ||| ||||| ||||| |||||
DB 16 TGCTCTCCGCTACCACCGTGCCACTCCAGCAGGGGGCGG 55

RESULT 15
US-11-244-330A-2131
; Sequence 2131, Application US/11244330A
; Publication No. US20060195932A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 2131
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700098705H1
US-11-244-330A-2131

Query Match      28.9%; Score 17.6; DB 7; Length 120;
Best Local Similarity 65.0%; Pred. No. 1e+04;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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DB 41 TGCTCTCCGCTACCACCGTGCCACTCCAGCAGGGGGCGG 80

Search completed: October 14, 2005, 19:38:23
Job time : 121 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:36:24 ; Search time 2007 Seconds
(without alignments)
605.382 Million cell updates/sec

Title: US-10-604-926A-4539

Perfect score: 19

Sequence: 1 ggagaagggtgggtgct 19

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1796954

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : GenEmbl.*

1: gb_env.*

2: gb_pat.*

3: gb_ph.*

4: gb_pl.*

5: gb_pr.*

6: gb_ro.*

7: gb_sta.*

8: gb_sy.*

9: gb_un.*

10: gb_vl.*

11: gb_ov.*

12: gb_hcg.*

13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	13.2	69.5	21	AR761712	Sequence
7	13.2	69.5	25	AR125125	Sequence
8	12.8	67.4	27	AR030170	Sequence
9	12.8	67.4	29	CS025768	Sequence
10	12.8	67.4	30	CS015778	Sequence
11	12.6	66.3	25	AX207085	Sequence
12	12.6	66.3	30	AX785961	Sequence
13	12.4	65.3	17	AR173370	Sequence
14	12.4	65.3	18	AR096649	Sequence
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22	12.4	65.3	22	2	E30525	Nucleic aci
23	12.4	65.3	24	2	CS210348	Sequence
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28	12.4	65.3	30	2	I26957	Sequence 6
29	12.4	65.3	30	2	AR306619	Sequence
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93	11.8	CQ622050	Sequence	166	11.6	61.1	19	2	BD273329	Adenoviru
94	11.8	CQ622051	Sequence	167	11.6	61.1	19	2	CS122992	Sequence
95	11.8	CQ622052	Sequence	168	11.6	61.1	19	2	CS155937	Sequence
96	11.8	AR463113	Sequence	C 169	11.6	61.1	19	2	CS155958	Sequence
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98	11.8	AR463115	Sequence	C 171	11.6	61.1	19	2	AR643612	Sequence
C 99	11.8	AR2333412	Sequence	172	11.6	61.1	19	2	AR650179	Sequence
100	11.8	I28584	Sequence 37	173	11.6	61.1	19	2	AR693667	Sequence
101	11.8	IS8746	Sequence 37	174	11.6	61.1	19	2	AX006536	Sequence
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105	11.8	AR156844	Sequence	C 178	11.6	61.1	19	5	S43670	S43670 NADH dehydr
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107	11.8	AR344270	Sequence	180	11.6	61.1	20	2	A76999	Sequence 43
108	11.8	AR489480	Sequence	C 181	11.6	61.1	20	2	AR067076	Sequence
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C 110	11.8	AX154090	Sequence	183	11.6	61.1	20	2	AR632371	Sequence
C 111	11.8	AX166297	Sequence	C 184	11.6	61.1	20	2	AR652615	Sequence
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136	11.8	AR468012	Sequence	C 209	11.4	60.0	17	2	BD254398	Regulatio
137	11.8	AR468013	Sequence	210	11.4	60.0	17	2	AR233644	Sequence
138	11.8	AR468014	Sequence	211	11.4	60.0	17	2	AR722135	Sequence
C 139	11.8	AR468015	Sequence	212	11.4	60.0	17	2	AX356513	Sequence
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C 141	11.8	AR037521	Sequence	C 214	11.4	60.0	17	2	AX498911	Sequence
C 142	11.8	AR062801	Sequence	C 215	11.4	60.0	17	2	AX498912	Sequence
C 143	11.8	AR087879	Sequence	C 216	11.4	60.0	17	2	AX498913	Sequence
C 144	11.8	AR091349	Sequence	C 217	11.4	60.0	17	2	AX498914	Sequence
C 145	11.8	AR118055	Sequence	C 218	11.4	60.0	17	2	AX498915	Sequence
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153	11.8	AR130634	Sequence	C 226	11.4	60.0	20	2	AR433559	Sequence
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157	11.8	BD189394	HCV Genom	C 230	11.4	60.0	21	2	AX154139	Sequence
C 158	11.8	AX694778	Sequence 13	231	11.4	60.0	22	2	AR122064	Sequence
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162	11.6	CS188104	Sequence	C 235	11.4	60.0	22	2	BD102264	Method of
163	11.6	AX481057	Sequence	236	11.4	60.0	22	2	BD232289	Productio
164	11.6	BD218785	Chimaeric	C 237	11.4	60.0	22	2	BD237447	Single nu

c 238	11.4	60.0	22	2	BD270511	Method. 7	311	11.2	58.9	20	2	AX451877	Sequence
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c 275	11.4	60.0	26	2	AR437295	Sequence	c 348	11.2	58.9	25	2	AX329416	Sequence
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c 278	11.4	60.0	28	2	AR076006	Sequence	351	11.2	58.9	25	2	AX783142	Sequence
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c 286	11.4	60.0	30	2	AX174867	Sequence	359	11.2	58.9	26	2	CS146489	Sequence
c 287	11.2	58.9	15	2	AX796723	Sequence	360	11.2	58.9	26	2	CS146521	Sequence
c 288	11.2	58.9	15	2	AR805762	Sequence	361	11.2	58.9	26	2	CS156176	Sequence
c 289	11.2	58.9	16	2	AX027205	Sequence	c 362	11.2	58.9	26	2	DD192999	NOVEL PRO
c 290	11.2	58.9	17	2	AX724690	Sequence	c 363	11.2	58.9	26	2	E39040	Non-reducin
c 291	11.2	58.9	17	2	AX729418	Sequence	c 364	11.2	58.9	26	2	AR197447	Sequence
c 292	11.2	58.9	17	2	AX782389	Sequence	c 365	11.2	58.9	26	2	AR259601	Sequence
c 293	11.2	58.9	17	2	AX782391	Sequence	c 366	11.2	58.9	26	2	AX207927	Sequence
c 294	11.2	58.9	18	2	AX811352	Sequence	367	11.2	58.9	27	2	E37265	Novel phys1
c 295	11.2	58.9	19	2	DD201267	RNA Inter	368	11.2	58.9	27	2	AR266307	Sequence
c 296	11.2	58.9	19	2	DD201390	RNA Inter	c 369	11.2	58.9	27	2	AR392189	Sequence
c 297	11.2	58.9	19	2	I78662	Sequence 17	c 370	11.2	58.9	27	2	AR392189	Sequence
c 298	11.2	58.9	20	2	AR037340	Sequence	371	11.2	58.9	27	2	AX30645	Sequence
c 299	11.2	58.9	20	2	AR040623	Sequence	372	11.2	58.9	27	2	AX105555	Sequence
c 300	11.2	58.9	20	2	AR100402	Sequence	c 373	11.2	58.9	27	2	AX329463	Sequence
c 301	11.2	58.9	20	2	AR130805	Sequence	c 374	11.2	58.9	28	2	CS063383	Sequence
c 302	11.2	58.9	20	2	AR150057	Sequence	c 375	11.2	58.9	28	2	CS081164	Sequence
c 303	11.2	58.9	20	2	BD227930	Anti1sense	c 376	11.2	58.9	28	2	DD177618	NUCLEIC A
c 304	11.2	58.9	20	2	CS173458	Sequence	377	11.2	58.9	28	2	AX046580	Sequence
c 305	11.2	58.9	20	2	CS173458	Sequence	c 378	11.2	58.9	28	2	AX404862	Sequence
c 306	11.2	58.9	20	2	CS173459	Sequence	c 379	11.2	58.9	28	2	AX799251	Sequence
c 307	11.2	58.9	20	2	I19634	Sequence 15	c 380	11.2	58.9	29	2	AX655758	Sequence
c 308	11.2	58.9	20	2	I20470	Sequence 49	c 381	11.2	58.9	30	2	A65658	Sequence 2
c 309	11.2	58.9	20	2	AR297477	Sequence	c 382	11.2	58.9	30	2	AR125803	Sequence
c 310	11.2	58.9	20	2	I72498	Sequence 82	c 383	11.2	58.9	30	2	BD187380	Inhibicio
					I72499	Sequence 83				30	2	I47215	Sequence 14

384	11..2	58..9	30	2	AR562672 Sequence	c 457	11	57..9	25	2	AR403906 Sequence
385	11	57..9	11	2	AR066200 Sequence	c 458	11	57..9	25	2	AR488650 Sequence
386	11	57..9	11	2	AR086457 Sequence	c 459	11	57..9	25	2	AR532791 Sequence
387	11	57..9	11	2	AR108744 Sequence	c 460	11	57..9	25	2	AR634134 Sequence
388	11	57..9	11	2	CQ832705 Sequence	c 461	11	57..9	25	2	AR634141 Sequence
389	11	57..9	11	2	CS058491 Sequence	c 462	11	57..9	25	2	AR708782 Sequence
390	11	57..9	11	2	AR241256 Sequence	c 463	11	57..9	25	2	AR772600 Sequence
391	11	57..9	11	2	AR281929 Sequence	c 464	11	57..9	25	2	AX127666 Sequence
392	11	57..9	11	2	AR368783 Sequence	c 465	11	57..9	25	2	AX127674 Sequence
393	11	57..9	11	2	AR610918 Sequence	c 466	11	57..9	25	2	AX140048 Sequence
394	11	57..9	11	2	AR643025 Sequence	c 467	11	57..9	25	2	AX140056 Sequence
395	11	57..9	11	2	AR758591 Sequence	c 468	11	57..9	25	2	AX521602 Sequence
396	11	57..9	12	2	AR030072 Sequence	c 469	11	57..9	25	2	AX610908 Sequence
397	11	57..9	13	2	AR030064 Sequence	c 470	11	57..9	26	2	BD078157 Modulator
398	11	57..9	17	2	BD258435 Regulation	c 471	11	57..9	26	2	BD078191 Modulator
399	11	57..9	19	2	AR005135 Sequence	c 472	11	57..9	26	2	BD260149 Screening
400	11	57..9	19	2	AR118500 Sequence	c 473	11	57..9	26	2	BD262473 Informati
401	11	57..9	19	2	AR214546 Sequence	c 474	11	57..9	26	2	AR700895 Sequence
402	11	57..9	19	2	AR278101 Sequence	c 475	11	57..9	26	2	AX037031 Sequence
403	11	57..9	19	2	AR279579 Sequence	c 476	11	57..9	26	2	AX037896 Sequence
404	11	57..9	19	2	AR568259 Sequence	c 477	11	57..9	27	2	AR168788 Sequence
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407	11	57..9	19	2	AR615343 Sequence	c 480	11	57..9	27	2	CS208122 Sequence
408	11	57..9	19	2	AR689962 Sequence	c 481	11	57..9	27	2	CS208130 Sequence
409	11	57..9	19	2	AX305145 Sequence	c 482	11	57..9	27	2	I27782 Sequence 14
410	11	57..9	20	2	AR100400 Sequence	c 483	11	57..9	27	2	AR200257 Sequence
411	11	57..9	20	2	AR150055 Sequence	c 484	11	57..9	27	2	AR204715 Sequence
412	11	57..9	20	2	AR173823 Sequence	c 485	11	57..9	27	2	AR262389 Sequence
413	11	57..9	20	2	AR173824 Sequence	c 486	11	57..9	27	2	AX128203 Sequence
414	11	57..9	20	2	BD227928 Ant.isense	c 487	11	57..9	27	2	AX460973 Sequence
415	11	57..9	20	2	CQ840052 Sequence	c 488	11	57..9	28	2	A98589 Sequence 14
416	11	57..9	20	2	CS039004 Sequence	c 489	11	57..9	28	2	DD210564 GENOMIC S
417	11	57..9	20	2	DD177416 Verificat	c 490	11	57..9	28	2	E38138 Method for
418	11	57..9	20	2	AR442481 Sequence	c 491	11	57..9	28	2	AR437131 Sequence
419	11	57..9	20	2	AR704105 Sequence	c 492	11	57..9	28	5	S90280 {deletion 1
420	11	57..9	20	2	AX805155 Sequence	c 493	11	57..9	28	5	S90283 {deletion 2
421	11	57..9	21	2	BD022423 Multi-fun	c 494	11	57..9	28	5	S90337 {deletion 1
422	11	57..9	21	2	BD262820 Method fo	c 495	11	57..9	29	2	BD095255 A chemoki
423	11	57..9	21	2	CS017965 Sequence	c 496	11	57..9	29	2	BD186073 Methods o
424	11	57..9	21	2	CS235527 Sequence	c 497	11	57..9	29	2	AR715087 Sequence
425	11	57..9	21	2	AR198750 Sequence	c 498	11	57..9	29	2	AR715088 Sequence
426	11	57..9	21	2	AR202254 Sequence	c 499	11	57..9	30	2	AR048180 Sequence
427	11	57..9	21	2	AR223256 Sequence	c 500	11	57..9	30	2	BD010718 Helicobac
428	11	57..9	21	2	AR263002 Sequence	c 501	11	57..9	30	2	BD267776 Potentiat
429	11	57..9	21	2	AR532790 Sequence	c 502	11	57..9	30	2	BD267810 Enhanceme
430	11	57..9	21	2	AR567801 Sequence	c 503	11	57..9	30	2	CS176205 Sequence
431	11	57..9	21	2	AR616414 Sequence	c 504	11	57..9	30	2	E14027 Probe. 7/19
432	11	57..9	21	2	AR722599 Sequence	c 505	11	57..9	30	5	HUMPLTP25
433	11	57..9	21	2	AX167173 Sequence	c 506	11	57..9	30	5	AX785962 Sequence
434	11	57..9	21	2	AX235480 Sequence	c 507	10..8	56..8	14	2	U37832 Human phosph
435	11	57..9	22	2	AX5399 Sequence 69	c 508	10..8	56..8	14	2	BD137817 Protein e
436	11	57..9	22	2	AR061204 Sequence	c 509	10..8	56..8	15	2	AR575807 Sequence 1
437	11	57..9	22	2	CQ760253 Sequence	c 510	10..8	56..8	15	2	AS0781 Sequence 2
438	11	57..9	22	2	DD176305 Verificat	c 511	10..8	56..8	15	2	AR109974 Sequence
439	11	57..9	22	2	AX804044 Sequence	c 512	10..8	56..8	15	2	AR109975 Sequence
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441	11	57..9	24	2	A04020 Sequence 47	c 514	10..8	56..8	15	2	I33988 Sequence 2
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443	11	57..9	24	2	CQ816817 Sequence	c 516	10..8	56..8	17	2	AR045385 Sequence
444	11	57..9	24	2	AX815865 Sequence	c 517	10..8	56..8	17	2	BD259257 Regulation
445	11	57..9	25	2	A71353 Sequence 4	c 518	10..8	56..8	17	2	BD266424 Universal
446	11	57..9	25	2	AR142053 Sequence	c 519	10..8	56..8	17	2	CQ617572 Sequence
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453	11	57..9	25	2	AR223257 Sequence	c 526	10..8	56..8	17	2	DD188174 Probe set
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455	11	57..9	25	2	I86778 Sequence 47	c 528	10..8	56..8	17	2	AR286483 Sequence
456	11	57..9	25	2	I95803 Sequence 47	c 529	10..8	56..8	17	2	I52437 Sequence 17

C 530	10.8	56.8	17	2	I94428	I94428 Sequence 59	C 603	10.8	56.8	23	2	AX107474	Sequence
C 531	10.8	56.8	17	2	AR398473	AR398473 Sequence	604	10.8	56.8	23	4	AJ719044	AJ719044 Sequence
C 532	10.8	56.8	17	2	AR458635	AR458635 Sequence	605	10.8	56.8	24	2	A57515	A57515 Sequence 7
C 533	10.8	56.8	17	2	AR458636	AR458636 Sequence	606	10.8	56.8	24	2	AR052981	Sequence
C 534	10.8	56.8	17	2	AR458637	AR458637 Sequence	607	10.8	56.8	24	2	BD229114	BD229114 Endogeneo
C 535	10.8	56.8	17	2	AR458638	AR458638 Sequence	608	10.8	56.8	24	2	CQ767675	Sequence
C 536	10.8	56.8	17	2	AR463112	AR463112 Sequence	609	10.8	56.8	24	2	CS016276	CS016276 Sequence
C 537	10.8	56.8	17	2	AR463116	AR463116 Sequence	C 610	10.8	56.8	24	2	CS158083	Sequence
C 538	10.8	56.8	17	2	AX215454	AX215454 Sequence	C 611	10.8	56.8	24	2	DD212175	DD212175 MODULATIO
C 539	10.8	56.8	17	2	AX215455	AX215455 Sequence	612	10.8	56.8	24	2	AR431789	AR431789 Sequence
C 540	10.8	56.8	17	2	AX215456	AX215456 Sequence	613	10.8	56.8	24	2	AR697473	Sequence
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C 545	10.8	56.8	18	2	AX923497	AX923497 Sequence	618	10.8	56.8	25	2	AR055503	Sequence
C 546	10.8	56.8	18	2	BD190823	BD190823 G-rich ol	619	10.8	56.8	25	2	AR055512	Sequence
C 547	10.8	56.8	18	2	BD190838	BD190838 G-rich ol	620	10.8	56.8	25	2	AR085386	Sequence
C 548	10.8	56.8	18	2	CQ784357	CQ784357 Sequence	621	10.8	56.8	25	2	AR085395	Sequence
C 549	10.8	56.8	18	2	DD162379	DD162379 Transgeni	C 622	10.8	56.8	25	2	CQ620501	Sequence
C 550	10.8	56.8	18	2	AR570260	AR570260 Sequence	C 623	10.8	56.8	25	2	CQ620502	Sequence
C 551	10.8	56.8	18	2	AX767745	AX767745 Sequence	C 624	10.8	56.8	25	2	CQ620503	Sequence
C 552	10.8	56.8	18	2	AX796219	AX796219 Sequence	C 625	10.8	56.8	25	2	CQ620504	Sequence
C 553	10.8	56.8	18	2	AX796220	AX796220 Sequence	C 626	10.8	56.8	25	2	CQ620505	Sequence
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C 555	10.8	56.8	19	2	DD192671	DD192671 Method fo	C 628	10.8	56.8	25	2	CQ620507	Sequence
C 556	10.8	56.8	19	2	AR295127	AR295127 Sequence	C 629	10.8	56.8	25	2	CQ620508	Sequence
C 557	10.8	56.8	19	2	AX404233	AX404233 Sequence	C 630	10.8	56.8	25	2	CQ620509	Sequence
C 558	10.8	56.8	19	2	AX477615	AX477615 Sequence	C 631	10.8	56.8	25	2	CQ620510	Sequence
C 559	10.8	56.8	19	2	AX482168	AX482168 Sequence	C 632	10.8	56.8	25	2	CQ620511	Sequence
C 560	10.8	56.8	19	2	AX505035	AX505035 Sequence	C 633	10.8	56.8	25	2	CQ620512	Sequence
C 561	10.8	56.8	19	2	AX511407	AX511407 Sequence	634	10.8	56.8	25	2	CQ626941	Sequence
C 562	10.8	56.8	19	2	AX659401	AX659401 Sequence	635	10.8	56.8	25	2	CQ626953	Sequence
C 563	10.8	56.8	19	2	AX721768	AX721768 Sequence	636	10.8	56.8	25	2	CQ862047	Sequence
C 564	10.8	56.8	20	2	A26760	A26760 Oligonucleo	637	10.8	56.8	25	2	CQ862090	Sequence
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C 566	10.8	56.8	20	2	AR126694	AR126694 Sequence	639	10.8	56.8	25	2	CQ866555	Sequence
C 567	10.8	56.8	20	2	BD143391	BD143391 Human bla	640	10.8	56.8	25	2	CQ890003	Sequence
C 568	10.8	56.8	20	2	BD226640	BD226640 Methods f	C 641	10.8	56.8	25	2	CS010247	Sequence
C 569	10.8	56.8	20	2	CQ754283	CQ754283 Sequence	C 642	10.8	56.8	25	2	CS122162	Sequence
C 570	10.8	56.8	20	2	CQ876459	CQ876459 Sequence	643	10.8	56.8	25	2	AR342808	Sequence
C 571	10.8	56.8	20	2	CQ975224	CQ975224 Sequence	644	10.8	56.8	25	2	AR441869	Sequence
C 572	10.8	56.8	20	2	CS011689	CS011689 Sequence	C 645	10.8	56.8	25	2	AR461564	Sequence
C 573	10.8	56.8	20	2	DD174360	DD174360 SELECTION	C 646	10.8	56.8	25	2	AR461565	Sequence
C 574	10.8	56.8	20	2	DD177122	DD177122 Verificat	C 647	10.8	56.8	25	2	AR461566	Sequence
C 575	10.8	56.8	20	2	E40690	E40690 Antihuman F	C 648	10.8	56.8	25	2	AR461567	Sequence
C 576	10.8	56.8	20	2	AR268255	AR268255 Sequence	C 649	10.8	56.8	25	2	AR461568	Sequence
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C 579	10.8	56.8	20	2	AR317237	AR317237 Sequence	C 652	10.8	56.8	25	2	AR461571	Sequence
C 580	10.8	56.8	20	2	AR453337	AR453337 Sequence	C 653	10.8	56.8	25	2	AR461572	Sequence
C 581	10.8	56.8	20	2	AR454806	AR454806 Sequence	C 654	10.8	56.8	25	2	AR461573	Sequence
C 582	10.8	56.8	20	2	AR652614	AR652614 Sequence	C 655	10.8	56.8	25	2	AR461574	Sequence
C 583	10.8	56.8	20	2	AX6664949	AX6664949 Sequence	C 656	10.8	56.8	25	2	AR461575	Sequence
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C 585	10.8	56.8	20	2	AX804861	AX804861 Sequence	658	10.8	56.8	25	2	AR468016	Sequence
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C 588	10.8	56.8	21	2	BD260882	BD260882 PCR cloni	661	10.8	56.8	25	2	AX194388	Sequence
C 589	10.8	56.8	21	2	BD269904	BD269904 Tumor nec	662	10.8	56.8	25	2	AX453028	Sequence
C 590	10.8	56.8	21	2	CQ774691	CQ774691 Sequence	C 663	10.8	56.8	26	2	CS077915	Sequence
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C 594	10.8	56.8	21	2	CS227039	CS227039 Sequence	C 667	10.8	56.8	28	2	A57793	Sequence 6
C 595	10.8	56.8	21	2	CS227040	CS227040 Sequence	668	10.8	56.8	28	2	AR120087	Sequence
C 596	10.8	56.8	21	2	I42191	I42191 Sequence 4	669	10.8	56.8	28	2	AR120088	Sequence
C 597	10.8	56.8	21	2	AR287735	AR287735 Sequence	C 670	10.8	56.8	28	2	AR120089	Sequence
C 598	10.8	56.8	21	2	AR381137	AR381137 Sequence	C 671	10.8	56.8	28	2	BD141804	BD141804 Novel G p
C 599	10.8	56.8	21	2	AR704961	AR704961 Sequence	C 672	10.8	56.8	28	2	BD174277	BD174277 Novel phi
C 600	10.8	56.8	21	2	AX023396	AX023396 Sequence	C 673	10.8	56.8	28	2	BD181755	BD181755 Novel G p
C 601	10.8	56.8	23	2	CS014378	CS014378 Sequence	C 674	10.8	56.8	28	2	CS144091	Sequence
C 602	10.8	56.8	23	2	CS150594	CS150594 Sequence	675	10.8	56.8	28	2	CS144092	Sequence

C 676	10.8	56.8	28	2	I41109	I41109 Sequence 12	C 749	10.6	55.8	20	2	CQ983702	CQ983702 Sequence
C 677	10.8	56.8	28	2	I41110	I41110 Sequence 13	C 750	10.6	55.8	20	2	CS130455	CS130455 Sequence
C 678	10.8	56.8	28	2	I41111	I41111 Sequence 14	C 751	10.6	55.8	20	2	CS130456	CS130456 Sequence
C 679	10.8	56.8	28	2	I41112	I41112 Sequence 15	C 752	10.6	55.8	20	2	CS256367	CS256367 Sequence
C 680	10.8	56.8	28	2	I41113	I41113 Sequence 16	C 753	10.6	55.8	20	2	DD174846	DD174846 THERAPEUT
C 681	10.8	56.8	29	2	BD081646	BD081646 Secreted	C 754	10.6	55.8	20	2	DD174870	DD174870 THERAPEUT
C 682	10.8	56.8	29	2	CS077900	CS077900 Sequence	C 755	10.6	55.8	20	2	DD174885	DD174885 THERAPEUT
C 683	10.8	56.8	29	2	CS077914	CS077914 Sequence	C 756	10.6	55.8	20	2	DD174927	DD174927 THERAPEUT
C 684	10.8	56.8	29	2	CS097981	CS097981 Sequence	C 757	10.6	55.8	20	2	DD175002	DD175002 THERAPEUT
C 685	10.8	56.8	29	2	CS097995	CS097995 Sequence	C 758	10.6	55.8	20	2	DD175032	DD175032 THERAPEUT
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C 690	10.8	56.8	30	2	AS0795	AS0795 Sequence 16	C 763	10.6	55.8	20	2	AR182693	AR182693 Sequence
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C 713	10.6	55.8	17	2	AX1794	AX1794 Sequence 4	C 786	10.6	55.8	20	2	AX740256	AX740256 Sequence
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C 720	10.6	55.8	18	2	AX698808	AX698808 Sequence	C 793	10.6	55.8	21	2	AR265306	AR265306 Sequence
C 721	10.6	55.8	19	2	CS014962	CS014962 Sequence	C 794	10.6	55.8	21	2	AR589353	AR589353 Sequence
C 722	10.6	55.8	19	2	CS015376	CS015376 Sequence	C 795	10.6	55.8	21	2	AR709643	AR709643 Sequence
C 723	10.6	55.8	19	2	AR240862	AR240862 Sequence	C 796	10.6	55.8	21	2	AX045693	AX045693 Sequence
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C 727	10.6	55.8	20	2	A79212	A79212 Sequence 49	C 800	10.6	55.8	21	2	AX304980	AX304980 Sequence
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C 732	10.6	55.8	20	2	AR074319	AR074319 Sequence	C 805	10.6	55.8	22	2	BD261048	BD261048 Assay for
C 733	10.6	55.8	20	2	AR074320	AR074320 Sequence	C 806	10.6	55.8	22	2	CS228241	CS228241 Sequence
C 734	10.6	55.8	20	2	AR076636	AR076636 Sequence	C 807	10.6	55.8	22	2	E36949	E36949 Human telom
C 735	10.6	55.8	20	2	AR078333	AR078333 Sequence	C 808	10.6	55.8	22	2	AR223442	AR223442 Sequence
C 736	10.6	55.8	20	2	AR098868	AR098868 Sequence	C 809	10.6	55.8	22	2	AR243470	AR243470 Sequence
C 737	10.6	55.8	20	2	AR173053	AR173053 Sequence	C 810	10.6	55.8	22	2	AR390626	AR390626 Sequence
C 738	10.6	55.8	20	2	BD003442	BD003442 A gene re	C 811	10.6	55.8	22	2	AR393240	AR393240 Sequence
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C 742	10.6	55.8	20	2	BD136817	BD136817 Artificia	C 815	10.6	55.8	23	2	BD185726	BD185726 Applicati
C 743	10.6	55.8	20	2	BD175178	BD175178 Method fo	C 816	10.6	55.8	23	2	BD245240	BD245240 Method of
C 744	10.6	55.8	20	2	BD175179	BD175179 Method fo	C 817	10.6	55.8	23	2	CQ798333	CQ798333 Sequence
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C 748	10.6	55.8	20	2			C 821	10.6	55.8	23	2	AX339382	AX339382 Sequence

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823	10.6	55.8	24	2	AR168045	Sequence	896	10.6	55.8	27	2	I24911	Sequence 54
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGTGGG 15
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Db 1 CGAGAAGGGGTGGG 15

RESULT 4
AR704960/c
LOCUS AR704960 22 bp DNA linear PAT 20-SEP-2005
DEFINITION Sequence 23 from patent US 6929912.
ACCESSION AR704960
VERSION AR704960.1 GI:75923278
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Guida, M., Hall, J., Petros, W.P., Vredenburg, J.J., Colvin, O.M. and Marks, J.R.
TITLE Methods for evaluating the ability to metabolize pharmaceuticals
JOURNAL Patent: US 6929912-A 23 16-AUG-2005;
Genaisance Pharmaceuticals, Inc. and Duke University; New Haven, CT

FEATURES
source Location/Qualifiers
1..22
/organism="unknown"
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ORIGIN
Query Match 70.5%; Score 13.4; DB 2; Length 22;
Best Local Similarity 93.3%; Pred. No. 6e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGTGGG 15
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Db 22 CGAGAAGGGGTGGG 8

RESULT 5
AR298092/c
LOCUS AR298092 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 9827 from patent US 6537751.
ACCESSION AR298092
VERSION AR298092.1 GI:31685376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 9827 25-MAR-2003;
Genet S.A.;;
FRX;

FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 69.5%; Score 13.2; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 7.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAAGGGGTGGTCT 19
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Db 18 GAGAAGGGGTAAGTCT 1

RESULT 6
AR761712

LOCUS AR761712 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 21 from patent US 6962776.
ACCESSION AR761712
VERSION AR761712.1 GI:83330324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kopecky, S.L., Goronsy, J.J. and Weyand, C.M.
TITLE Methods and materials for evaluating cardiovascular conditions
JOURNAL Patent: US 6962776-A 21 08-NOV-2005;
Mayo Foundation for Medical Education and Research; Rochester, MN

FEATURES
source Location/Qualifiers
1..21
/organism="unknown"
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ORIGIN
Query Match 69.5%; Score 13.2; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 7.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAAGGGGTGGTCT 19
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Db 2 CGAAGGGGGGGTCT 19

RESULT 7
AR125125
LOCUS AR125125 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 12 from patent US 6177086.
ACCESSION AR125125
VERSION AR125125.1 GI:14111187
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Riley, L.W., Nathan, C.F. and Ehrh, S.
TITLE DNA molecule conferring on Mycobacterium tuberculosis resistance against antimicrobial reactive oxygen and nitrogen intermediates
JOURNAL Patent: US 6177086-A 12 23-JAN-2001;
Location/Qualifiers
source 1..25
/organism="unknown"
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ORIGIN
Query Match 69.5%; Score 13.2; DB 2; Length 25;
Best Local Similarity 83.3%; Pred. No. 7.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGTGGTGC 18
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Db 1 GGGATGGCGGTGGTGC 18

RESULT 8
AR030170/c
LOCUS AR030170 27 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 359 from patent US 5861244.
ACCESSION AR030170
VERSION AR030170.1 GI:5943384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 359 19-JAN-1999;
Location/Qualifiers

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source
1. .27
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 2; Length 27;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGGTG 17
Db 17 GAGATGGGGTGGGAG 2

RESULT 9
CS025768/c
LOCUS CS025768 29 bp DNA linear PAT 03-MAR-2005
DEFINITION Sequence 20 from Patent WO2005014029.
ACCESSION CS025768
VERSION CS025768.1 GI:60496425
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Onichtchouk, D.
TITLE Use of dg008, dg065, dg210 or dg 239 secreted protein products for preventing and treating pancreatic diseases and/or obesity and/or metabolic syndrome
JOURNAL Patent: WO 2005014029-A 20 17-FEB-2005;
DEVELOPMENT DeveloGen Aktiengesellschaft fuer entwicklungsbiologische Forschung (DE)
FEATURES
source Location/Qualifiers
1. .29
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: probe mouse D0239 Tagman probe"

ORIGIN

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 2; Length 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGTGGGTGC 18
Db 20 AGTAGGGTGTGGGTGC 5

RESULT 10
CS015778/c
LOCUS CS015778 30 bp DNA linear PAT 11-FEB-2005
DEFINITION Sequence 5 from Patent WO2005007198.
ACCESSION CS015778
VERSION CS015778.1 GI:59675351
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Chang, X. J.
TITLE Disease specific agents for diagnostics and therapeutics
JOURNAL Patent: WO 2005007198-A 5 27-JAN-2005;
ATTORNEY Atrogen, Inc. (US)
FEATURES
source Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Synthetic oligonucleotide"

ORIGIN

1. .27
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match
Best Local Similarity 67.4%; Score 12.8; DB 2; Length 30;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGTGGGTGC 18
Db 23 AGAGGGGAGTGGGTGC 8

RESULT 11
AX207085/c
LOCUS AX207085 25 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 38 from Patent WO0153476.
ACCESSION AX207085
VERSION AX207085.1 GI:15394882
KEYWORDS Nicotiana tabacum (common tobacco)
SOURCE Nicotiana tabacum
ORGANISM Nicotiana tabacum
REFERENCE
AUTHORS Bruce, W. B. and Niu, X.
TITLE Novel plant promoters and methods of use
JOURNAL Patent: WO 0153476-A 38 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
1. .25
/organism="Nicotiana tabacum"
/mol_type="unassigned DNA"
/db_xref="taxon:4097"

ORIGIN

Query Match
Best Local Similarity 66.3%; Score 12.6; DB 2; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTGCT 19
Db 25 GGAGAAGGAGTGAAGCT 7

RESULT 12
AX785961/c
LOCUS AX785961 30 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 470 from Patent WO03050299.
ACCESSION AX785961
VERSION AX785961.1 GI:32953581
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cullen, P. and Seedorf, U.
TITLE Method for analysing hereditary masculine infertility
JOURNAL Patent: WO 03050299-A 470 19-JUN-2003;
OGHAM GmbH (DE)
FEATURES
source Location/Qualifiers
1. .30
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match
Best Local Similarity 66.3%; Score 12.6; DB 2; Length 30;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTGCT 19
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Db 23 GCAGGAGGAGGGGGGCT 5

RESULT 13
LOCUS AR173370/c
DEFINITION Sequence 4 from patent US 6303847.
ACCESSION AR173370
VERSION AR173370.1 GI:17912861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kawaka,A. and Ebinuma,H.
TITLE DNA encoding a transcription factor controlling phenylpropanoid biosynthesis pathway
JOURNAL Patent: US 6303847-A 4 16-OCT-2001;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAAGGGGGTGGTG 17
|||||
Db 17 GAAGGGGGTGGTG 4

RESULT 14
LOCUS AR096649
DEFINITION Sequence 33 from patent US 6008048.
ACCESSION AR096649
VERSION AR096649.1 GI:10025634
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia,B.P. and Cowser,L.M.
TITLE Antisense inhibition of EGR-1 expression
JOURNAL Patent: US 6008048-A 33 28-DEC-1999;
FEATURES
source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGGTGG 14
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Db 5 CGAGAAGGGGGTGG 18

RESULT 15
LOCUS CS095398/c
DEFINITION Sequence 90 from Patent WO2005045035.
ACCESSION CS095398
VERSION CS095398.1 GI:66951985
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.

AUTHORS Mcswiggen,J., Chowrira,B.M. and Haerberli,P.
TITLE RNA interference mediated inhibition of NOGO and NOGO receptor gene expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045035-A 90 19-MAY-2005;
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Target Sequence/siNA sense region"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGGTGG 14
|||||
Db 17 CGAGATGGGGTGG 4

RESULT 16
LOCUS CS095497
DEFINITION Sequence 189 from Patent WO2005045035.
ACCESSION CS095497
VERSION CS095497.1 GI:66952084
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.

AUTHORS Mcswiggen,J., Chowrira,B.M. and Haerberli,P.
TITLE RNA interference mediated inhibition of NOGO and NOGO receptor gene expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045035-A 189 19-MAY-2005;
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: siNA antisense region"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGGTGG 14
|||||
Db 3 CGAGATGGGGTGG 16

RESULT 17
LOCUS AX826824/c
DEFINITION Sequence 46 from Patent WO03072823.
ACCESSION AX826824
VERSION AX826824.1 GI:39752338
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.

AUTHORS Grandchamp,B. and Mentre,F.
TITLE Method for in vitro detection of cancers by highlighting allelic imbalances in insertion/deletion markers
JOURNAL Patent: WO 03072823-A 46 04-SEP-2003;
ASSISTANCE PUBLIQUE, HOPITAUX DE PARIS (FR)

FEATURES	source		Location/Qualifiers		1. .20		/organism="synthetic construct"		/mol_type="unassigned DNA"		/db_xref="taxon:32630"		/note="SEQUENCE DESCRIPTION artificielle: amorce"									
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	QY		1 GGAGAGGGGGTGG 14																			
	Db		16 GGAGAGGGGGTGG 3																			
	RESULT 18		AR529043		Sequence 246 from patent US 6727063.		21 bp		DNA		linear		PAT 08-OCT-2004		LOCUS		AR529043		Accession		AR529043	
	DEFINITION		AR529043		Version		AR529043.1		GI:53917480		Keywords		Unknown.		ORGANISM		Unclassified.		REFERENCE		Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.	
	AUTHORS		TITLE		Single nucleotide polymorphisms in genes		Patent: US 6727063-A 246 27-APR-2004;		Millennium Pharmaceuticals, Inc. and Whitehead Institute for Biomedical Research; Cambridge, MA		JOURNAL		Biomedical Research; Cambridge, MA		FEATURES		source		1. .21		/organism="unknown"	
	ORIGIN		Query Match		65.3%;		Score 12.4;		DB 2;		Length 21;		Matches 13;		Conservative 1;		Mismatches 2;		Indels 0;		Gaps 0;	
	QY		4 GAAGGGGGTGGTCT 19																			
	Db		3 GAAGAGGGGGTGGTACT 18																			
FEATURES	source		AX095068		Sequence 246 from Patent WO0118250.		21 bp		DNA		linear		PAT 30-MAR-2001		LOCUS		AX095068		Accession		AX095068	
	DEFINITION		AX095068		Version		AX095068.1		GI:13511271		Keywords		Homo sapiens (human)		ORGANISM		Homo sapiens		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		REFERENCE	
	AUTHORS		TITLE		Single nucleotide polymorphisms in genes		Patent: WO 0118250-A 246 15-MAR-2001.		WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)		JOURNAL		Pharmaceuticals, Inc. (US)		FEATURES		source		1. .21		/organism="Homo sapiens"	

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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match          65.3%; Score 12.4; DB 2; Length 22;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGGT 16
    ||||| |||||
Db 22 AGAAGTGGGTGGGT 9

RESULT 22
E30525/c
LOCUS      22 bp DNA linear PAT 18-JUN-2001
DEFINITION Nucleic acid primer for distinguishing eel species and method for
            distinguishing eel species by using the same.
ACCESSION  E30525
VERSION    JP 1999276179-A/3.
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified sequences.
REFERENCE  1 (bases 1 to 22)
AUTHORS   Toshihiro,T. and Masatoshi,K.
TITLE     Nucleic acid primer for distinguishing eel species and method for
            distinguishing eel species by using the same
JOURNAL    Patent: JP 1999276179-A 3 12-OCT-1999;
COMMENT    SHIZUOKA INST OF SCI & TECHNOL,SRL INC

PN JP 1999276179-A/3
PD 12-OCT-1999
PF 30-MAR-1998 JP 1998102209
PR
PT
TOSHIHIRO TSUNEYOSHI,MASATOSHI KAJI
FC C12N15/09,A01K61/00,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..22
FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..22
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match          65.3%; Score 12.4; DB 2; Length 22;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGGT 16
    ||||| |||||
Db 22 AGAAGTGGGTGGGT 9

RESULT 23
CS210348/c
LOCUS      24 bp DNA linear PAT 15-DEC-2005
DEFINITION Sequence 170 from Patent WO2005111232.
ACCESSION  CS210348
VERSION    CS210348.1 GI:83687387
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS   Hermeking,H.
TITLE     Silencing of tumor-suppressive genes by cpG-methylation in prostate
            cancer
JOURNAL    Patent: WO 2005111232-A 170 24-NOV-2005;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V.

/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match          65.3%; Score 12.4; DB 2; Length 24;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAAGGGGGTGGGTG 17
    ||||| |||||
Db 22 GAAGGGGGTGGGTG 9

RESULT 24
CS210350/c
LOCUS      24 bp DNA linear PAT 15-DEC-2005
DEFINITION Sequence 172 from Patent WO2005111232.
ACCESSION  CS210350
VERSION    CS210350.1 GI:83687389
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS   Hermeking,H.
TITLE     Silencing of tumor-suppressive genes by cpG-methylation in prostate
            cancer
JOURNAL    Patent: WO 2005111232-A 172 24-NOV-2005;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V.
            Berlin (DE)

FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match          65.3%; Score 12.4; DB 2; Length 24;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAAGGGGGTGGGTG 17
    ||||| |||||
Db 22 GAAGGGGGTGGGTG 9

RESULT 25
AX548302/c
LOCUS      25 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 226 from Patent WO0240716.
ACCESSION  AX548302
VERSION    AX548302.1 GI:25813336
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS   Palm,K.
TITLE     Profiling tumor specific markers for the diagnosis and treatment of
            neoplastic disease
JOURNAL    Patent: WO 0240716-A 226 23-MAY-2002;
            Cemines, LLC (US)

FEATURES
source
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

ORIGIN
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Query Match 65.3%; Score 12.4; DB 2; Length 25;
Best Local Similarity 92.9%; Pred. No. 2e+05; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAGAAGGGGGTGGG 15
|||||
Db 14 GAGAAGGGCGTGGG 1

RESULT 26
AR658517/c
LOCUS 27 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 191 from patent US 6897053.
ACCESSION AR658517
VERSION AR658517.1 GI:67593124
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS O'Donnell,M.E. and Yurieva,O.
TITLE Enzymes derived from thermophilic organisms that function as a
chromosomal replicase, preparation and use thereof
JOURNAL Patent: US 6897053-A 191 24-MAY-2005;
Rockefeller University; New York, NY
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 27;
Best Local Similarity 92.9%; Pred. No. 2e+05; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGG 14
|||||
Db 19 GGAGAAGGTGGTG 6

RESULT 27
BD171352
LOCUS 30 bp DNA linear PAT 18-FEB-2003
DEFINITION Method for predicting sensitivity to Helicobacter Pylori by
analysis of gene polymorphism of secretion type gene, Lewis gene,
interleukin 1B and myeloperoxidase gene.

ACCESSION BD171352
VERSION BD171352.1 GI:28412642
KEYWORDS JP 2002218996-A/5.
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Hamajima,N., Ikehara,Y., Tatematsu,M. and Nishibara,S.
TITLE Method for predicting sensitivity to Helicobacter Pylori by
analysis of gene polymorphism of secretion type gene, Lewis gene,
interleukin 1B and myeloperoxidase gene
Patent: JP 2002218996-A 5 06-AUG-2002;
JOURNAL NOBUYUKI HAMAJIMA,YUZURU IKEHARA,MASAMORI TATEMATSU,SHOKO NISHIHARA
COMMENT OS Unidentified
PN JP 2002218996-A/5
PD 06-AUG-2002
PF 23-JAN-2001 JP 2001014871
PI NOBUYUKI HAMAJIMA,YUZURU IKEHARA,MASAMORI TATEMATSU,SHOKO NISHIHARA
PC C12Q1/68,C12N15/09,C12N15/00
CC Method for predicting sensitivity to Helicobacter Pylori by
analysis of
CC gene polymorphism of secretion type gene, Lewis gene, CC
interleukin 1B and
CC myeloperoxidase gene
FH Key Location/Qualifiers

FT source 1..30
/organism='Unidentified'.
FEATURES
source
1..30
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAAGGGGGTGGTG 17
|||||
Db 5 GCAGGGGGTGGTG 18

RESULT 28
I26957/c
LOCUS 30 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 6 from patent US 5561224.
ACCESSION I26957
VERSION I26957.1 GI:1606827
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Rosenfeld,M.G. and Anderson,B.
TITLE Transcription factor for regulation of the development of skin and
hair
JOURNAL Patent: US 5561224-A 6 01-OCT-1996;
FEATURES
source
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Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGG 14
|||||
Db 24 GGAGAAGGAGGTGG 11

RESULT 29
AR306619/c
LOCUS 30 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 10 from patent US 6548642.
ACCESSION AR306619
VERSION AR306619.1 GI:31696821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 10 15-APR-2003;
Ohio University; Athens, OH
FEATURES
source
1..30
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 30
LOCUS AR306628/c 30 bp DNA
DEFINITION Sequence 38 from patent US 6548642.
ACCESSION AR306628
VERSION AR306628.1 GI:31696830
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kielszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 38 15-APR-2003;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 31
LOCUS AR306629 30 bp DNA
DEFINITION Sequence 39 from patent US 6548642.
ACCESSION AR306629
VERSION AR306629.1 GI:31696831
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kielszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 39 15-APR-2003;
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 32
LOCUS AR340054/c 30 bp DNA
DEFINITION Sequence 10 from patent US 6570062.
ACCESSION AR340054
VERSION AR340054.1 GI:33731348
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kielszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6570062-A 39 27-MAY-2003;
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 33
LOCUS AR340063/c 30 bp DNA
DEFINITION Sequence 38 from patent US 6570062.
ACCESSION AR340063
VERSION AR340063.1 GI:33731357
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kielszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL Patent: US 6570062-A 38 27-MAY-2003;
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 34
LOCUS AR340064 30 bp DNA
DEFINITION Sequence 39 from patent US 6570062.
ACCESSION AR340064
VERSION AR340064.1 GI:33731358
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kielszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL Patent: US 6570062-A 39 27-MAY-2003;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
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/mol_type="unassigned DNA"

ORIGIN
Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGG 14
    ||||| ||||| |||||
Db 11 GGAGATGGGGTGG 24

RESULT 35
AR412123/c
LOCUS AR412123 30 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 10 from patent US 6639050.
ACCESSION AR412123
VERSION AR412123.1 GI:40166767
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
JOURNAL Patent: US 6639050-A 10 28-OCT-2003;
FEATURES
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Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGG 14
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RESULT 36
AR412132/c
LOCUS AR412132 30 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 38 from patent US 6639050.
ACCESSION AR412132
VERSION AR412132.1 GI:40166776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
JOURNAL Patent: US 6639050-A 38 28-OCT-2003;
FEATURES
  Location/Qualifiers
  source
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Db 29 GGAGATGGGGTGG 16

RESULT 37
AR412133
LOCUS AR412133 30 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 39 from patent US 6639050.
ACCESSION AR412133
VERSION AR412133.1 GI:40166777
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
JOURNAL Patent: US 6639050-A 39 28-OCT-2003;
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ORIGIN
Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 11 GGAGATGGGGTGG 24

RESULT 38
AR782390
LOCUS AR782390 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 721 from Patent WO03050284.
ACCESSION AR782390
VERSION AX782390.1 GI:32950239
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 721 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
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QY 1 GGAGAAGGGGTGGTGG 17
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Db 1 GGAGAAGGGGTGGTGG 17

RESULT 39
AR016234/c
LOCUS AR016234 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 122 from patent US 5776682.
ACCESSION AR016234
VERSION AR016234.1 GI:3972511
KEYWORDS
SOURCE Unknown.
```


ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS First, M. Kent., Agoulmik, A. I. and Muallem, A.
TITLE Male infertility Y-deletion detection battery
JOURNAL Patent: US 5776682-A 122 07-JUL-1998;
FEATURES Location/Qualifiers
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QY 1 GGAGGAGGGGTGGGTG 17
Db 18 GAAGAAGGGGTGGGTG 2

RESULT 40
LOCUS AR035649/c 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 81 from patent US 5871920.
ACCESSION AR035649
VERSION AR035649.1 GI:5952317
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Page, D. C. and Reijo, R.
TITLE Daz, a gene associated with azoospermia
JOURNAL Patent: US 5871920-A 81 16-FEB-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 82.4%; Pred. No. 2.4e+05;
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QY 1 GGAGGAGGGGTGGGTG 17
Db 18 GAAGAAGGGGTGGGTG 2

RESULT 41
LOCUS AR060627/c 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5840708.
ACCESSION AR060627
VERSION AR060627.1 GI:5987077
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weiss, B.
TITLE Administration of oligonucleotides antisense to dopamine receptor
JOURNAL MRNA for diagnosis and treatment of Neurological pathologies
FEATURES Patent: US 5840708-A 10 24-NOV-1998;
source 1..20
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/mol_type="unassigned DNA"

ORIGIN

Query Match 64.2%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.5e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGGAGGGGTGGGTG 17
Db 17 GGAGATGGAGGTAGGTG 1

RESULT 42
LOCUS CQ786920 20 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 97 from Patent WO2004021010.
ACCESSION CQ786920
VERSION CQ786920.1 GI:45721912
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura, Y. and Furukawa, Y.
TITLE Method of diagnosing colon and gastric cancers
JOURNAL Patent: WO 2004021010-A 97 11-MAR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the president of the university of Tokyo (JP)
FEATURES Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGGTGCT 19
Db 18 AGAAGGAGGTGGGGCCT 2

RESULT 43
LOCUS CQ800189 20 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 14 from Patent WO2004031411.
ACCESSION CQ800189
VERSION CQ800189.1 GI:46849107
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura, Y. and Katagiri, T.
TITLE Genes and polypeptides relating to human pancreatic cancers
JOURNAL Patent: WO 2004031411-A 14 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by The president of the University of Tokyo (JP)
FEATURES Location/Qualifiers
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/note="Artificially synthesized primer sequence for RT-PCR"

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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGGTGCT 19
Db 18 AGAAGGAGGTGGGGCCT 2

RESULT 44
CQ875013/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

1
CQ875013
Sequence 35 from Patent WO2004076623.
CQ875013
CQ875013.1 GI:52748106
synthetic construct
synthetic construct
other sequences; artificial sequences.
Nakamura, Y. and Furukawa, Y.
Compositions and methods of inhibiting cell growth
Patent: WO 2004076623-A 35 10-SEP-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by The
President of the University of Tokyo (JP)
Location/Qualifiers
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Query Match 64.2%; Score 12.2; DB 2; Length 20;
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Qy 3 AGAAGGGGGTGGGTGCT 19
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RESULT 45
CS012032/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

1
CS012032
Sequence 1957 from Patent WO2005007144.
CS012032
CS012032.1 GI:59671847
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Hakonarson, H., Gurney, M.E. and Halapi, E.
Methods of diagnosis and treatment for asthma based on haplotype
association
Patent: WO 2005007144-A 1957 27-JAN-2005;
Decode Genetics EHF. (IS)
Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 64.2%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGCT 19
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Db 18 ACAAGTGGGTGGGTGCT 2

RESULT 46
CS163806/c
LOCUS
DEFINITION

1
CS163806
Sequence 17 from Patent WO2005083086.
CS163806
CS163806.1 GI:76360380
synthetic construct
synthetic construct
other sequences; artificial sequences.
Nakamura, Y.
Epha4 as therapeutic target of prc and pdaca
Patent: WO 2005083086-A 17 09-SEP-2005;
The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)
Location/Qualifiers
1. .20
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="An artificially synthesized primer sequence"

Query Match 64.2%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGCT 19
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Db 18 AGAAGGAGGTGGGCCT 2

RESULT 47
CS174584/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

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CS174584
Sequence 15 from Patent WO2005090398.
CS174584
CS174584.1 GI:77625448
synthetic construct
synthetic construct
other sequences; artificial sequences.
Nakamura, Y.
Genes and polypeptides relating to prostate cancers
Patent: WO 2005090398-A 15 29-SEP-2005;
The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)
Location/Qualifiers
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/note="An artificially synthesized primer sequence"

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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGCT 19
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Db 18 AGAAGGAGGTGGGCCT 2

RESULT 48
CS174749/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

1
CS174749
Sequence 28 from Patent WO2005090572.
CS174749
CS174749.1 GI:77625601
synthetic construct
synthetic construct
other sequences; artificial sequences.
Nakamura, Y.
Compositions and methods for treating pancreatic cancer

JOURNAL Patent: WO 2005090572-A 28 29-SEP-2005;
The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)
FEATURES
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 18 AGAAGGGGTGGGCCT 2

RESULT 49
AR315974/c
LOCUS AR315974 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6511 from patent US 6559294.
ACCESSION AR315974
VERSION AR315974.1 GI:31709400
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6511 06-MAY-2003;
Genset, S.A.;;
FRX;

FEATURES
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ORIGIN
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QY 2 GAGAGGGGTGGTGTC 18
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Db 19 GAGAAGGGGTAGGAGC 3

RESULT 50
AR565351/c
LOCUS AR565351 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 29 from patent US 6767705.
ACCESSION AR565351
VERSION AR565351.1 GI:53981207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Roninson, I.B., Dokmanovic, M. and Chang, B.-D.
TITLE Reagents and methods for identifying and modulating expression of
genes regulated by retinoids
JOURNAL Patent: US 6767705-A 29 27-JUL-2004;
The Board of Trustees of the University of Illinois; Urbana, IL

FEATURES
source
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ORIGIN

Query Match 64.2%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. NO. 2.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGNAGGGGTGGGTG 17
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Db 19 GAAGAAGGGGGAGGATG 3

Search completed: October 14, 2006, 20:12:31
Job time : 2043 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:34:51 ; Search time 300 Seconds
(without alignments)
441.576 Million cell updates/sec

Title: US-10-604-926A-4539
Perfect score: 19
Sequence: 1 ggagaagggtgggtgct 19
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 4443654

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq.8.*
1: Geneseqn1980s.*
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3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
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7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
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12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

'Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	14.2	74.7	30	8	Abz70091 Human chr
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	13.8	72.6	20	13	Adk23254 Acyl-coen
	13.8	72.6	20	13	Adk23371 Acyl-coen
6	13.8	72.6	20	13	Adk23372 Acyl-coen
7	13.8	72.6	20	13	Adk23389 Acyl-coen
8	13.8	72.6	20	13	Adk23389 Acyl-coen
C	13.8	72.6	20	15	Aef42976 Mesoblast
	13.8	72.6	21	12	Adn00574 Murine ad
	13.8	72.6	21	14	Ady38715 Mouse adi
C	13.8	72.6	23	14	Adw43979 Human MOD
C	13.8	70.5	19	14	Adz87881 Early gro
C	13.4	70.5	19	14	Adz88055 Early gro
15	13.4	70.5	19	14	Aeb43635 Novel hum
C	13.4	70.5	19	14	Aeb43461 Novel hum
C	13.4	70.5	22	6	Aad45780 Human pro
C	13.2	69.5	18	3	Aaz75471 Human bia

Adi57107 Oryza min	20	12	69.5	13.2	ADI57107
AbA00323 cDNA enco	21	6	69.5	13.2	ABAO0323
Aav72586 NOXR1 cDN	25	2	69.5	13.2	AAV72586
Ado12772 Single mu	30	12	69.5	13.2	ADO12772
Ado12782 Single mu	30	12	69.5	13.2	ADO12782
Abc22092 Oligonuel	13	5	68.4	13	ABC22092
Abc22093 Oligonuel	13	5	68.4	13	ABC22093
Aag99298 Multi-dru	20	2	67.4	12.8	AAQ99298
Aag99297 Multi-dru	20	2	67.4	12.8	AAQ99297
Aag99296 Multi-dru	20	2	67.4	12.8	AAQ99296
Aad48534 Chicken l	20	8	67.4	12.8	AAD48534
Acc59333 Human MIZ	20	9	67.4	12.8	ACC59333
Adk23418 Acyl-coen	20	13	67.4	12.8	ADK23418
Adk23492 Acyl-coen	20	13	67.4	12.8	ADK23492
Aaq99295 Multi-dru	22	2	67.4	12.8	AAQ99295
Ady33449 CFTR gene	23	14	67.4	12.8	ADY33449
Aav15574 Primer fo	24	2	67.4	12.8	AAV15574
Abk51637 Human ABC	26	6	67.4	12.8	ABK51637
Adz15700 Mutagenic	26	13	67.4	12.8	ADZ15700
Aax14972 Triple he	27	2	67.4	12.8	AAX14972
Adw58930 Mouse DG2	29	14	67.4	12.8	ADW58930
Adw28628 HER-2 spl	30	14	67.4	12.8	ADW28628
Adf93340 Human TER	19	10	66.3	12.6	ADF93340
Adf93594 Human TER	19	10	66.3	12.6	ADF93594
Adg64570 Human G72	19	10	66.3	12.6	ADG64570
Adg64626 Human G72	19	10	66.3	12.6	ADG64626
Aeb17755 G72 siRNA	19	14	66.3	12.6	AEB17755
Aeb17699 G72 siRNA	19	14	66.3	12.6	AEB17699
Aeb15820 Human tel	19	14	66.3	12.6	AEB15820
Aeb15597 Human tel	19	14	66.3	12.6	AEB15597
Aac66150 21-hydrox	23	3	66.3	12.6	AAC66150
Aef42944 Human ABC	23	15	66.3	12.6	AEF42944
Aaq06157 Chicken o	24	2	66.3	12.6	AAQ06157
Aah42746 A promote	25	4	66.3	12.6	AAH42746
Aas22192 Human COL	25	5	66.3	12.6	AAS22192
Aef31348 Cotton AR	25	14	66.3	12.6	AEF31348
Aaz25859 Human pol	29	2	66.3	12.6	AAZ25859
Ad42608 Human inf	30	10	66.3	12.6	ADD42608
Aaz44155 Human EGR	18	3	65.3	12.4	AZ44155
Aec06517 NOGO rece	19	14	65.3	12.4	AEC06517
Aec06418 NOGO rece	19	14	65.3	12.4	AEC06418
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Aed33358 Human NOG	19	14	65.3	12.4	AED33358
Aef75992 Human NOG	19	15	65.3	12.4	AEF75992
Aef76091 Human NOG	19	15	65.3	12.4	AEF76091
Aaz05108 PCR prime	20	2	65.3	12.4	AZ05108
Adc06823 Cancer-re	20	10	65.3	12.4	ADE06823
Adc01537 Novel mut	21	13	65.3	12.4	ADT01537
Aav52673 Hepatocyt	22	2	65.3	12.4	AAV52673
Aaz31903 PCR prime	22	2	65.3	12.4	AZ31903
Aaz47796 Anguilla	22	3	65.3	12.4	AZ47796
Adg92552 Human hep	22	13	65.3	12.4	ADS92552
Aea78703 Human SCN	22	14	65.3	12.4	AEA78703
Aee09587 SMARCAL 9	24	14	65.3	12.4	AEE09587
Aee09589 SMARCAL 9	24	14	65.3	12.4	AEE09589
Abt03705 Human Nlx	25	6	65.3	12.4	ABT03705
Adj67961 T. thermo	27	12	65.3	12.4	ADJ67961
Adj68173 T. thermo	27	12	65.3	12.4	ADJ68173
Adk01251 DNA polym	27	12	65.3	12.4	ADK01251
Adj79470 T. thermo	27	12	65.3	12.4	ADJ79470
Adj84910 T. thermo	27	12	65.3	12.4	ADJ84910
Adm77698 DNA polym	27	12	65.3	12.4	ADM77698
Adm66365 T. thermo	27	12	65.3	12.4	ADM66365
Ado04418 T. thermo	27	12	65.3	12.4	ADO04418
Adp82495 Therms t	27	12	65.3	12.4	ADP82495
Adg15702 T. thermo	27	13	65.3	12.4	ADG15702
Ady55193 T. thermo	27	14	65.3	12.4	ADY55193
Adz76769 T. thermo	27	14	65.3	12.4	ADZ76769
Aea24777 T. thermop	27	14	65.3	12.4	AEA24777
Aea34200 T. thermop	27	14	65.3	12.4	AEA34200
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Abq80635 Secretor	30	6	65.3	12.4	ABQ80635

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C 93	12.4	65.3	30	6	ABL51739	Ab151739 Hydroxypr	166	12	63.2	22	15	AEF05498	Aef05498 Bisulfite
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C 97	12.4	65.3	30	13	ADU09144	Adu09144 Ser-Hyp4	c 170	11.8	62.1	17	5	ADU02233	Adv02233 Human BAC
C 98	12.4	65.3	17	10	ADF62817	Adf62817 Human PCC	c 171	11.8	62.1	17	5	ADV03316	Adv03316 Human BAC
C 99	12.2	64.2	18	2	AAT68368	Aat68368 Loc1-spec	172	11.8	62.1	17	6	ABN06799	Abn06799 Human GDM
C 100	12.2	64.2	18	2	AXA01506	Axa01506 Primer ST	173	11.8	62.1	17	6	ABN06800	Abn06800 Human GDM
C 101	12.2	64.2	18	3	AAZ92565	Aaz92565 Human Y-s	174	11.8	62.1	17	6	ABN06798	Abn06798 Human GDM
C 102	12.2	64.2	18	13	ADT01610	Adt01610 Novel mut	175	11.8	62.1	17	13	ACN69889	Acn69889 Human GDM
C 103	12.2	64.2	19	10	ADG68684	Adg68684 DNA ampli	176	11.8	62.1	17	13	ACN69890	Acn69890 Human GDM
C 104	12.2	64.2	20	2	AAQ688205	Aaq688205 Human D2	177	11.8	62.1	17	13	ACN69888	Acn69888 Human GDM
C 105	12.2	64.2	20	2	AAT86561	Aat86561 Human D2	c 178	11.8	62.1	18	5	AAS43549	Aas43549 Corneodes
C 106	12.2	64.2	20	2	AAZ97185	Aaz97185 Primer us	c 179	11.8	62.1	18	5	ADL18253	Adl18253 Antisense
C 107	12.2	64.2	20	5	AAZ22302	Aaz22302 Human COL	c 180	11.8	62.1	19	2	AAZ56945	Aaz56945 HIV-1 pro
C 108	12.2	64.2	20	5	AAS22301	Aas22301 Human COL	c 181	11.8	62.1	19	14	AEA42783	Aea42783 Human WNT
C 109	12.2	64.2	20	6	ADZ24940	Adz24940 Antisense	c 182	11.8	62.1	19	14	AEA42620	Aea42620 Human WNT
C 110	12.2	64.2	20	10	ABZ87731	Abz87731 Human oli	183	11.8	62.1	19	14	AEC25862	Aec25862 Human all
C 111	12.2	64.2	20	11	ABD23961	Abd23961 Human cal	184	11.8	62.1	19	14	AEC28228	Aec28228 Human all
C 112	12.2	64.2	20	12	ADL64441	Adl64441 Human U6s	185	11.8	62.1	19	15	AEE65444	Aee65444 Human vit
C 113	12.2	64.2	20	12	ADM96980	Adm96980 Human pan	c 186	11.8	62.1	19	15	AAE65188	Aee65188 Human vit
C 114	12.2	64.2	20	12	ADP11917	Adp11917 Set 2 rig	c 187	11.8	62.1	20	3	AAA66894	Aaa66894 Dog genom
C 115	12.2	64.2	20	13	ADR67729	Adr67729 Genomic D	c 188	11.8	62.1	20	4	RAH23483	Rah23483 Human MEK
C 116	12.2	64.2	20	14	ADM83302	Adm83302 MAP3K9 ma	c 189	11.8	62.1	20	6	RAH34758	Rah34758 Human MEK
C 117	12.2	64.2	20	14	AEC46225	Aec46225 Primer fo	190	11.8	62.1	20	13	ADK23370	Adk23370 Acyl-coen
C 118	12.2	64.2	20	14	ABD14984	Abd14984 Human snR	c 191	11.8	62.1	20	13	ADK23468	Adk23468 Acyl-coen
C 119	12.2	64.2	20	14	AED17711	Aed17711 Human snR	c 192	11.8	62.1	20	14	ADM44009	Adm44009 Human MOD
C 120	12.2	64.2	20	15	AE663417	Aee663417 Human snR	c 193	11.8	62.1	20	15	AE878274	Aee78274 Human dop
C 121	12.2	64.2	20	15	AEF74439	Aef74439 Human snR	194	11.8	62.1	20	15	AE878276	Aee78276 Human dop
C 122	12.2	64.2	21	6	ABS66907	Abs66907 Human MRP	195	11.8	62.1	20	15	AE878277	Aee78277 Human dop
C 123	12.2	64.2	21	6	ABS66906	Abs66906 Human MRP	196	11.8	62.1	20	15	AE878273	Aee78273 Human dop
C 124	12.2	64.2	21	8	ADZ49478	Adz49478 Second PC	197	11.8	62.1	20	15	AE878275	Aee78275 Human dop
C 125	12.2	64.2	21	12	ADP29168	Adp29168 Human sec	198	11.8	62.1	21	2	AAT64846	Aat64846 CMV immed
C 126	12.2	64.2	21	14	ADZ25719	Adz25719 HIV-1 Tat	199	11.8	62.1	21	2	AAZ22068	Aaz22068 PCR prime
C 127	12.2	64.2	21	14	AEC24185	Aec24185 Human all	200	11.8	62.1	21	2	AAH41879	Aah41879 Cytomegal
C 128	12.2	64.2	21	14	AEC26551	Aec26551 Human all	201	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
C 129	12.2	64.2	22	2	AAT11034	Aat11034 Antisense	202	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
C 130	12.2	64.2	22	2	AAT10288	Aat10288 RNA compo	203	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
C 131	12.2	64.2	22	2	AAF58870	Aaf58870 Human met	204	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
C 132	12.2	64.2	22	4	AAF58876	Aaf58876 Human met	c 205	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
C 133	12.2	64.2	22	4	AAF58878	Aaf58878 Human met	c 206	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
C 134	12.2	64.2	22	4	AAF58878	Aaf58878 Human met	c 207	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
C 135	12.2	64.2	23	13	ADS19194	Ads19194 PCR class	c 208	11.8	62.1	22	2	AAZ22539	Aaz22539 Human MMP
C 136	12.2	64.2	23	14	ADW08913	Adw08913 Canine be	c 209	11.8	62.1	22	2	AAZ22539	Aaz22539 Human MMP
C 137	12.2	64.2	24	6	ABN74968	Abn74968 Human MNR	c 210	11.8	62.1	22	10	ADF94328	Adf94328 Murine neu
C 138	12.2	64.2	25	10	ADF63568	Adf63568 Human PCC	c 211	11.8	62.1	23	4	ABH74156	Abh74156 Human neu
C 139	12.2	64.2	25	10	ADF63566	Adf63566 Human PCC	c 212	11.8	62.1	23	4	ABH74156	Abh74156 Human neu
C 140	12.2	64.2	25	10	ADF63562	Adf63562 Human PCC	213	11.8	62.1	24	2	AAV09032	Aav09032 Human Na+
C 141	12.2	64.2	25	10	ADF63567	Adf63567 Human PCC	214	11.8	62.1	24	4	AAZ21703	Aaz21703 Imperfect
C 142	12.2	64.2	25	10	ADF63561	Adf63561 Human PCC	215	11.8	62.1	24	6	ABQ02013	Abq02013 Imperfect
C 143	12.2	64.2	25	10	ADF63564	Adf63564 Human PCC	216	11.8	62.1	24	6	ABQ02013	Abq02013 Imperfect
C 144	12.2	64.2	25	10	ADF63565	Adf63565 Human PCC	c 217	11.8	62.1	24	6	ABQ07946	Abq07946 Oligonuc1
C 145	12.2	64.2	25	10	ADF63560	Adf63560 Human PCC	c 218	11.8	62.1	24	6	ABQ07946	Abq07946 Oligonuc1
C 146	12.2	64.2	25	10	ADF63563	Adf63563 Human PCC	c 219	11.8	62.1	24	6	ABQ07987	Abq07987 Oligonuc1
C 147	12.2	64.2	26	2	AAT60163	Aat60163 Collagen	c 220	11.8	62.1	24	13	ADT78185	Adt78185 Human D2
C 148	12.2	64.2	26	2	AAZ77401	Aaz77401 Human tel	221	11.8	62.1	25	6	ABN11693	Abn11693 Human GDM
C 149	12.2	64.2	26	3	AAZ98711	Aaz98711 Collagen	222	11.8	62.1	25	6	ABN11693	Abn11693 Human GDM
C 150	12.2	64.2	27	12	ADJ14687	Adj14687 Debrisoqu	223	11.8	62.1	25	6	ABN11694	Abn11694 Human GDM
C 151	12.2	64.2	27	12	ADO60789	Ado60789 Human deb	224	11.8	62.1	25	6	ABN11694	Abn11694 Human GDM
C 152	12.2	64.2	27	14	AEC89953	Aec89953 CYP2D6 ge	225	11.8	62.1	25	6	ABN11696	Abn11696 Human GDM
C 153	12.2	64.2	29	3	AAZ04666	Aaz04666 Polymorph	226	11.8	62.1	25	6	ABN11695	Abn11695 Human GDM
C 154	12.2	64.2	29	9	ACC85464	Acc85464 T thermoh	227	11.8	62.1	25	6	ABN11699	Abn11699 Human GDM
C 155	12.2	64.2	30	2	AAZ98021	Aaz98021 VEGF 2'-N	228	11.8	62.1	25	6	ABN11700	Abn11700 Human GDM
C 156	12.2	64.2	30	2	AAZ23112	Aaz23112 Human CD4	229	11.8	62.1	25	6	ABN11700	Abn11700 Human GDM
C 157	12.2	64.2	30	6	AAZ41207	Aaz41207 HIV-1 env	230	11.8	62.1	25	6	ABN11690	Abn11690 Human GDM
C 158	12.2	64.2	30	7	ADY31410	Ady31410 Human CDC	231	11.8	62.1	25	6	ABN11692	Abn11692 Human GDM
C 159	12.2	64.2	30	7	ADY36798	Ady36798 CDC2L1 fo	232	11.8	62.1	25	6	ABN11698	Abn11698 Human GDM
C 160	12.2	64.2	30	9	ACC85466	Acc85466 T thermoh	233	11.8	62.1	25	6	ABN11697	Abn11697 Human GDM
C 161	12.2	64.2	30	14	ADY01830	Ady01830 PCR prime	234	11.8	62.1	25	6	ABN11691	Abn11691 Human GDM
C 162	12.2	63.2	15	6	ABA96072	Abas96072 CYP8B1 al	235	11.8	62.1	25	13	ACN74781	Acn74781 Human GDM
C 163	12.2	63.2	17	3	AAF06236	Aaf06236 Hammerhea	236	11.8	62.1	25	13	ACN74782	Acn74782 Human GDM
C 164	12.2	63.2	20	10	ADD20323	Add20323 Oreochrom	237	11.8	62.1	25	13	ACN74780	Acn74780 Human GDM

238	11.8	62.1	25	13	ACN74784	Acn74784 Human GDM	C 311	11.6	61.1	21	13	ADT88487	Adt88487 Vasoactiv
239	11.8	62.1	25	13	ACN74786	Acn74786 Human GDM	C 312	11.6	61.1	21	14	ADZ87553	Adz87553 DNA methy
240	11.8	62.1	25	13	ADT99600	Adt99600 Quadruple	C 313	11.6	61.1	21	14	ADZ77235	Adz77235 Reverse p
241	11.8	62.1	25	13	ADT92593	Adt92593 Quadruple	C 314	11.6	61.1	21	15	AEF40164	Aef40164 Dengue vi
242	11.8	62.1	26	2	AAQ99939	AAq99939 Mouse WTS	C 315	11.6	61.1	22	2	AAQ01725	AAq01725 Human typ
243	11.8	62.1	26	2	AAQ00732	AAq00732 Multiple	C 316	11.6	61.1	22	10	ADJ33160	Adj33160 Primer se
244	11.8	62.1	26	2	AAV72306	AAv72306 Pl6 promo	C 317	11.6	61.1	23	5	AAF62511	Aaf62511 CDKN2A ex
245	11.8	62.1	26	2	AAV53846	AAv53846 Nucleotid	C 318	11.6	61.1	23	10	ADQ76833	Adq76833 Pfiesteri
246	11.8	62.1	26	2	AAV11265	AAv11265 Human MTS	C 319	11.6	61.1	24	4	AAI65243	AAi65243 Human pro
247	11.8	62.1	26	2	AAx40771	AAx40771 Oligonuc	C 320	11.6	61.1	24	6	ABK91194	ABk91194 Human U1
248	11.8	62.1	26	2	AAV70610	AAv70610 Probe use	C 321	11.6	61.1	24	6	ABS56309	ABs56309 Rice chro
249	11.8	62.1	26	3	AA95558	AA95558 Mouse Pl6	C 322	11.6	61.1	24	10	ADH16989	ADh16989 Mouse mon
250	11.8	62.1	26	3	AA955247	AA955247 Zea mays	C 323	11.6	61.1	24	12	ADO10733	Ado10733 Single mu
251	11.8	62.1	26	3	AAZ48797	AAz48797 PCR prime	C 324	11.6	61.1	24	12	ADO10785	Ado10785 Single mu
252	11.8	62.1	26	3	AAZ39996	AAz39996 PCR prime	C 325	11.6	61.1	24	12	ADQ09925	Adq09925 Mouse RT-
253	11.8	62.1	26	3	AA39380	AA39380 Mouse Pl6	C 326	11.6	61.1	24	14	ADW22719	ADw22719 Transposo
254	11.8	62.1	26	3	AA311190	AA311190 Mouse mul	C 327	11.6	61.1	24	14	ADY72807	ADy72807 Neomycin
255	11.8	62.1	26	4	AA58198	AA58198 Oligonuc	C 328	11.6	61.1	25	2	AAI35207	AAi35207 Neomycin
256	11.8	62.1	26	4	AA502591	AA502591 PCR prime	C 329	11.6	61.1	25	2	AAI16986	AAi16986 Primer #2
257	11.8	62.1	26	4	AA04739	AA04739 Alternati	C 330	11.6	61.1	25	9	ACI37385	ACi37385 Human m1c
258	11.8	62.1	26	4	AA04739	AA04739 Alternati	C 331	11.6	61.1	25	9	ACI77545	ACi77545 Human m1c
259	11.8	62.1	26	4	AA04739	AA04739 Alternati	C 332	11.6	61.1	25	9	ACC84797	ACC84797 Nucleotid
260	11.8	62.1	27	2	AA95879	AA95879 Competito	C 333	11.6	61.1	25	10	AA55668	AA55668 Bovine vi
261	11.8	62.1	27	4	AA021692	AA021692 Imperfect	C 334	11.6	61.1	26	12	ADL23290	ADl23290 GMCSF-Gas
262	11.8	62.1	27	4	AA021705	AA021705 Imperfect	C 335	11.6	61.1	27	6	ABS66909	ABs66909 Human MRP
263	11.8	62.1	27	4	AA021702	AA021702 Imperfect	C 336	11.6	61.1	27	6	ABS66908	ABs66908 Human MRP
264	11.8	62.1	27	4	AA021699	AA021699 Imperfect	C 337	11.6	61.1	27	6	ABS68769	ABs68769 Archaeogl
265	11.8	62.1	28	2	AAQ31105	AAq31105 Probe 74	C 338	11.6	61.1	27	8	ADE53128	ADe53128 PEN-1 rel
266	11.8	62.1	28	6	AAQ35016	AAq35016 Mismatche	C 339	11.6	61.1	27	8	ACF62504	ACf62504 Cancer ba
267	11.8	62.1	28	9	AD01886	AD01886 Mouse car	C 340	11.6	61.1	27	8	ADB21175	ADb21175 MRP1 base
268	11.8	62.1	28	10	ADB71625	ADb71625 Mouse car	C 341	11.6	61.1	27	10	ADB88264	ADb88264 Human UGT
269	11.8	62.1	28	12	ADH23328	ADh23328 Human GAT	C 342	11.6	61.1	27	10	ADB97247	ADb97247 Human MRP
270	11.8	62.1	29	3	AA32384	AA32384 H. vulgar	C 343	11.6	61.1	27	10	ADB92438	ADb92438 Human MRP
271	11.8	62.1	30	4	AAH91290	AAh91290 Human inf	C 344	11.6	61.1	27	14	ABE87355	ABe87355 Archaeogl
272	11.6	61.1	18	6	ABT04100	ABt04100 Human VEG	C 345	11.6	61.1	27	14	ABE76623	ABe76623 Maize Bra
273	11.6	61.1	18	8	ACD06057	ACd06057 Human VEG	C 346	11.6	61.1	27	14	ABE76623	ABe76623 Maize Bra
274	11.6	61.1	18	9	ACD19279	ACd19279 Human VEG	C 347	11.6	61.1	27	14	ABE76624	ABe76624 Maize Bra
275	11.6	61.1	18	14	ACE51722	ACE51722 Antisense	C 348	11.6	61.1	27	14	ABE76622	ABe76622 Maize Bra
276	11.6	61.1	18	14	ACE55570	ACE55570 Human VEG	C 349	11.6	61.1	28	10	ADK71330	ADk71330 Drug-tole
277	11.6	61.1	18	15	AAE10252	AAe10252 Human VEG	C 350	11.6	61.1	28	14	ABE36488	ABe36488 Multifunc
278	11.6	61.1	19	2	AAZ06728	AAz06728 Antisense	C 351	11.6	61.1	28	14	ABE36526	ABe36526 Multifunc
279	11.6	61.1	19	3	AAZ60424	AAz60424 PCR prime	C 352	11.6	61.1	29	2	AAV58366	AAv58366 Probe for
280	11.6	61.1	19	3	AAZ37936	AAz37936 Adenovira	C 353	11.6	61.1	29	12	ADL23301	ADl23301 GM-CSF up
281	11.6	61.1	19	3	AA91780	AA91780 Inhibin B	C 354	11.6	61.1	29	12	ADL23301	ADl23301 GM-CSF up
282	11.6	61.1	19	5	AA88825	AA88825 Ad5 hexon	C 355	11.6	61.1	30	13	ADV25245	ADv25245 Rice rubi
283	11.6	61.1	19	10	ADE27501	ADe27501 Stearoyl-	C 356	11.6	61.1	30	14	AEA28546	AEa28546 nptii tra
284	11.6	61.1	19	10	ADE27211	ADe27211 Stearoyl-	C 357	11.6	61.1	30	14	AE58912	AE58912 Human ost
285	11.6	61.1	19	14	ADZ20451	ADz20451 Adenoviru	C 358	11.6	61.1	30	14	AE58912	AE58912 Human ost
286	11.6	61.1	19	14	ABE08591	ABe08591 Human ade	C 359	11.4	60.0	13	5	ABC22094	ABc22094 Oligonuc
287	11.6	61.1	19	14	ABE58639	ABe58639 Human ost	C 360	11.4	60.0	13	5	ABC81987	ABc81987 Oligonuc
288	11.6	61.1	19	14	ABE58639	ABe58639 Human ost	C 361	11.4	60.0	13	5	ABC34318	ABc34318 Oligonuc
289	11.6	61.1	19	14	ABE52176	ABe52176 Human SCD	C 362	11.4	60.0	13	5	ABC22095	ABc22095 Oligonuc
290	11.6	61.1	19	14	ABE51886	ABe51886 Human SCD	C 363	11.4	60.0	13	5	ABC81986	ABc81986 Oligonuc
291	11.6	61.1	19	14	ABE53337	ABe53337 Human hai	C 364	11.4	60.0	13	5	ABC34319	ABc34319 Oligonuc
292	11.6	61.1	19	14	ABE53336	ABe53336 Human hai	C 365	11.4	60.0	13	5	ABC34319	ABc34319 Oligonuc
293	11.6	61.1	19	14	ABE53339	ABe53339 Human hai	C 366	11.4	60.0	13	12	ADM76188	ADm76188 NEPHA gen
294	11.6	61.1	20	2	AAQ82424	AAq82424 Chromosom	C 367	11.4	60.0	14	6	ABQ73006	ABq73006 Human liv
295	11.6	61.1	20	2	AAQ32535	AAq32535 Primer fo	C 368	11.4	60.0	14	12	ADM76189	ADm76189 NEPHA gen
296	11.6	61.1	20	3	AA111329	AA111329 Human TRP	C 369	11.4	60.0	15	4	AAF46341	AAf46341 IGFBP2 ol
297	11.6	61.1	20	5	AA017452	AA017452 Human TNF	C 370	11.4	60.0	15	4	AAF46340	AAf46340 IGFBP2 ol
298	11.6	61.1	20	8	AB53068	AB53068 P75NTR ge	C 371	11.4	60.0	15	6	AA99365	AA99365 Aldehyde
299	11.6	61.1	20	10	ACC00618	ACC00618 Human CAP	C 372	11.4	60.0	15	6	AAAC70181	AAa70181 Single nu
300	11.6	61.1	20	10	ADH88546	ADh88546 Single nu	C 373	11.4	60.0	17	3	AAF02086	AAf02086 Hammerhea
301	11.6	61.1	20	10	ADA66475	ADa66475 Transform	C 374	11.4	60.0	17	3	AAF02086	AAf02086 Hammerhea
302	11.6	61.1	20	10	ADA66475	ADa66475 Transform	C 375	11.4	60.0	17	3	AAF02085	AAf02085 Hammerhea
303	11.6	61.1	20	13	ADS73957	ADs73957 Human TNF	C 376	11.4	60.0	17	3	AAF02085	AAf02085 Hammerhea
304	11.6	61.1	20	13	ADT00840	ADt00840 Novel mut	C 377	11.4	60.0	17	5	AAV02092	AAv02092 Human TER
305	11.6	61.1	21	6	ABS66905	ABs66905 Human MRP	C 378	11.4	60.0	17	5	ABL55546	ABl55546 Oligonuc
306	11.6	61.1	21	6	ABS66904	ABs66904 Human MRP	C 379	11.4	60.0	17	6	ABL55545	ABl55545 Oligonuc
307	11.6	61.1	21	11	ADJ13140	ADj13140 Human DNA	C 380	11.4	60.0	17	6	ABV78976	ABv78976 Human HTP
308	11.6	61.1	21	11	ADJ13105	ADj13105 Human DNA	C 381	11.4	60.0	17	6	ABV78976	ABv78976 Human HTP
309	11.6	61.1	21	12	ADO25173	ADo25173 MCAW mRNA	C 382	11.4	60.0	17	6	ABV78972	ABv78972 Human HTP
310	11.6	61.1	21	13	ADR47012	ADr47012 Dengue vi	C 383	11.4	60.0	17	6	ABV78974	ABv78974 Human HTP

C 384	11.4	60.0	17	6	ABV78973	Abv78973 Human HTP	C 457	11.4	60.0	24	10	ADC68835	Adc68835 Human PRO
C 385	11.4	60.0	17	6	ABV78975	Abv78975 Human HTP	C 458	11.4	60.0	24	10	ADC62895	Adc62895 Human PRO
C 386	11.4	60.0	17	12	ADP03206	Adp03206 Allele sp	C 459	11.4	60.0	24	10	ADC67960	Adc67960 Human PRO
C 387	11.4	60.0	17	15	AEF55485	Aef55485 Human gen	C 460	11.4	60.0	24	10	ADC41280	Adc41280 Human PRO
C 388	11.4	60.0	18	6	AAH74510	Aah74510 PCR prime	C 461	11.4	60.0	24	10	ADC67335	Adc67335 Human PRO
C 389	11.4	60.0	18	6	ABL45137	Abi45137 Human chr	C 462	11.4	60.0	24	10	ADC62271	Adc62271 Human PRO
C 390	11.4	60.0	19	6	ABQ74948	Abq74948 Medane re	C 463	11.4	60.0	24	10	ADC41904	Adc41904 Human PRO
C 391	11.4	60.0	19	9	ACH66546	Ach66546 Antisense	C 464	11.4	60.0	24	10	ADC49273	Adc49273 Human PRO
C 392	11.4	60.0	19	13	ADR12295	Adr12295 15-lipox	C 465	11.4	60.0	24	10	ADRE35327	Adre35327 Human PRO
C 393	11.4	60.0	19	13	ADR75668	Adr75668 Human apo	C 466	11.4	60.0	24	10	ADRE16441	Adre16441 Human PRO
C 394	11.4	60.0	19	13	ADR78286	Adr78286 Human apo	C 467	11.4	60.0	24	10	ADD730356	Add730356 Human PRO
C 395	11.4	60.0	19	13	ADT82729	Adt82729 Apolipop	C 468	11.4	60.0	24	10	ADD72414	Add72414 Human PRO
C 396	11.4	60.0	19	13	ADT80111	Adt80111 Apolipop	C 469	11.4	60.0	24	10	ADBE40351	Adbe40351 5' TET an
C 397	11.4	60.0	19	14	AEBS0994	Aeb50994 Human ADA	C 470	11.4	60.0	24	10	ADE17065	Adel7065 Human PRO
C 398	11.4	60.0	19	14	AEBS0798	Aeb50798 Human ADA	C 471	11.4	60.0	24	10	ADE17079	Adel7079 Human PRO
C 399	11.4	60.0	20	2	AAQ920782	Aaq92082 Erythro	C 472	11.4	60.0	24	10	ADGS2836	Adgs2836 Human PRO
C 400	11.4	60.0	20	2	AAQ74112	Aaq74112 Human ery	C 473	11.4	60.0	24	10	ADG60156	Adg60156 Human PRO
C 401	11.4	60.0	20	2	AAQ96882	Aaq96882 PCR prime	C 474	11.4	60.0	24	10	ADI60916	Adi60916 Human PRO
C 402	11.4	60.0	20	2	AAQ96879	Aaq96879 PCR prime	C 475	11.4	60.0	24	10	ACD42625	Acda42625 Secreted
C 403	11.4	60.0	20	3	AAQ98282	Aaq98282 Human MSH	C 476	11.4	60.0	24	12	ADBE48573	Adbe48573 Human PRO
C 404	11.4	60.0	20	6	ABK14871	Abk14871 Human TCF	C 477	11.4	60.0	24	12	ADBE9674	Adbe9674 Human PRO
C 405	11.4	60.0	20	10	ADE94296	Ade94296 Human Epo	C 478	11.4	60.0	24	12	ADFE1314	Adfe1314 Human PRO
C 406	11.4	60.0	20	10	ABZ84914	Abz84914 Human oli	C 479	11.4	60.0	24	12	ADFA4006	Adfa4006 Human PRO
C 407	11.4	60.0	20	11	ABD21144	Abd21144 Human tra	C 480	11.4	60.0	24	12	ADFA45802	Adfa45802 Human PRO
C 408	11.4	60.0	20	12	ADQ78193	Adq78193 PCR prime	C 481	11.4	60.0	24	12	ADFA24198	Adfa24198 Human PRO
C 409	11.4	60.0	20	14	AEC25118	Aec25118 Human all	C 482	11.4	60.0	24	12	ADFA40630	Adfa40630 Human PRO
C 410	11.4	60.0	20	14	AEC27484	Aec27484 Human all	C 483	11.4	60.0	24	12	ADFA23574	Adfa23574 Human PRO
C 411	11.4	60.0	20	14	AED33220	Aed13220 Human FLJ	C 484	11.4	60.0	24	12	ADFA33557	Adfa33557 Human PRO
C 412	11.4	60.0	20	15	AEF23151	Aef23151 Protein t	C 485	11.4	60.0	24	12	ADFA27024	Adfa27024 Human PRO
C 413	11.4	60.0	21	3	AAE62576	Aae62576 Human alp	C 486	11.4	60.0	24	12	ADFA27660	Adfa27660 Human PRO
C 414	11.4	60.0	21	6	ABK12845	Abk12845 5' SST fo	C 487	11.4	60.0	24	12	ADFA41254	Adfa41254 Human PRO
C 415	11.4	60.0	21	11	ADJ13245	Adj13245 Human DNA	C 488	11.4	60.0	24	12	ADFA32933	Adfa32933 Human PRO
C 416	11.4	60.0	21	14	ADM97087	Adm97087 HuAFP CDN	C 489	11.4	60.0	24	12	ADFA25299	Adfa25299 Human PRO
C 417	11.4	60.0	22	2	AXX25642	Axx25642 EPO-fusio	C 490	11.4	60.0	24	12	ADFA26400	Adfa26400 Human PRO
C 418	11.4	60.0	22	2	AXX25703	Axx25703 Human ery	C 491	11.4	60.0	24	12	ADFA34189	Adfa34189 Human PRO
C 419	11.4	60.0	22	3	AAA49965	Aaa49965 Primer 13	C 492	11.4	60.0	24	12	ADFA46436	Adfa46436 Human PRO
C 420	11.4	60.0	22	4	AAI66680	Aai66680 Human CET	C 493	11.4	60.0	24	12	ADG504412	Adg504412 Human PRO
C 421	11.4	60.0	22	8	ADA00206	Ada00206 Mouse and	C 494	11.4	60.0	24	12	ADGA49788	Adga49788 Human PRO
C 422	11.4	60.0	22	13	ADR83213	Adr83213 Human mir	C 495	11.4	60.0	24	12	ADG51660	Adg51660 Human PRO
C 423	11.4	60.0	22	13	ADR83367	Adr83367 Human Pax	C 496	11.4	60.0	24	12	ADGA9164	Adga9164 Human PRO
C 424	11.4	60.0	22	14	ADX04735	Adx04735 Antisense	C 497	11.4	60.0	24	12	ADGA48540	Adga48540 Human PRO
C 425	11.4	60.0	22	14	ADX04110	Adx04110 Human mat	C 498	11.4	60.0	24	12	ADGS1036	Adgs1036 Human PRO
C 426	11.4	60.0	22	14	ADY30955	Ady30955 Micro RNA	C 499	11.4	60.0	24	12	ADGS58980	Adgs58980 Human PRO
C 427	11.4	60.0	22	14	ABE79516	Abey79516 Human hsa	C 500	11.4	60.0	24	12	ADG62436	Adg62436 Human neu
C 428	11.4	60.0	22	14	ABE79210	Abey79210 Human mic	C 501	11.4	60.0	24	12	ADH25461	Adh25461 Human PRO
C 429	11.4	60.0	22	14	AEC36268	Aec36268 Nucleotid	C 502	11.4	60.0	24	12	ADM17238	Adm17238 Human PRO
C 430	11.4	60.0	22	14	AED53439	Aed53439 Human tar	C 503	11.4	60.0	24	12	ADL07072	Adl07072 Human PRO
C 431	11.4	60.0	22	14	AEEO4350	Aee04350 Human mir	C 504	11.4	60.0	24	13	ADT93928	Adt93928 Human PRO
C 432	11.4	60.0	22	15	AEF60787	Aef60787 Mouse mic	C 505	11.4	60.0	24	13	ADU50194	Adu50194 PRO866 fo
C 433	11.4	60.0	23	2	AAH58191	Aah58191 Primer fo	C 506	11.4	60.0	24	14	ADM49473	Adm49473 PRO866 fo
C 434	11.4	60.0	23	4	AAH50124	Aah50124 Bacterial	C 507	11.4	60.0	24	14	ADW49473	Adw49473 Soybean a
C 435	11.4	60.0	23	10	ADF39467	Adf39467 HNRNP gen	C 508	11.4	60.0	24	14	ADW80970	Adw80970 Human HTP
C 436	11.4	60.0	23	12	ADK98297	Adk98297 Primer of	C 509	11.4	60.0	25	6	ABV80980	Abv80980 Human HTP
C 437	11.4	60.0	24	2	AAQ88799	Aaq88799 Oligo PM3	C 510	11.4	60.0	25	6	ABV80972	Abv80972 Human HTP
C 438	11.4	60.0	24	2	AAZ34092	Aaz34092 Human PRO	C 511	11.4	60.0	25	6	ABV80979	Abv80979 Human HTP
C 439	11.4	60.0	24	3	AAC58520	Aac58520 Human PRO	C 512	11.4	60.0	25	6	ABV80974	Abv80974 Human HTP
C 440	11.4	60.0	24	3	AAC78753	Aac78753 Human PRO	C 513	11.4	60.0	25	6	ABV80973	Abv80973 Human HTP
C 441	11.4	60.0	24	3	AAA49767	Aaa49767 Human PRO	C 514	11.4	60.0	25	6	ABV80975	Abv80975 Human HTP
C 442	11.4	60.0	24	3	AAC61743	Aac61743 Primer fo	C 515	11.4	60.0	25	6	ABV80977	Abv80977 Human HTP
C 443	11.4	60.0	24	8	ACA63660	Ac63660 Novel hum	C 516	11.4	60.0	25	6	ABV80981	Abv80981 Human HTP
C 444	11.4	60.0	24	8	ACA71824	Ac71824 Human PRO	C 517	11.4	60.0	25	6	ABV80976	Abv80976 Human HTP
C 445	11.4	60.0	24	8	ACB92464	Abx92464 Human PRO	C 518	11.4	60.0	25	6	ABV80978	Abv80978 Human HTP
C 446	11.4	60.0	24	8	ACN66205	Acn66205 Human sec	C 519	11.4	60.0	25	6	ABV80979	Abv80979 Human HTP
C 447	11.4	60.0	24	9	ADA24778	Ada24778 Secreted	C 520	11.4	60.0	25	6	ABV80977	Abv80977 Human HTP
C 448	11.4	60.0	24	9	ACD29806	Ac29806 Novel hum	C 521	11.4	60.0	25	6	ABV80981	Abv80981 Human HTP
C 449	11.4	60.0	24	9	ADA12439	Ada12439 Human sec	C 522	11.4	60.0	25	6	ABV80969	Abv80969 Human HTP
C 450	11.4	60.0	24	9	ACD29221	Ac29221 Novel hum	C 523	11.4	60.0	25	6	ABV80971	Abv80971 Human HTP
C 451	11.4	60.0	24	10	ADB73745	Adb73745 Human PRO	C 524	11.4	60.0	25	6	ABV80976	Abv80976 Human HTP
C 452	11.4	60.0	24	10	ADB76461	Adb76461 Human PRO	C 525	11.4	60.0	25	6	ABV80978	Abv80978 Human HTP
C 453	11.4	60.0	24	10	ADC43887	Adc43887 Human PRO	C 526	11.4	60.0	25	8	AAD48617	Aad48617 Mycobacte
C 454	11.4	60.0	24	10	ADC61647	Adc61647 Human PRO	C 527	11.4	60.0	25	9	ACI03341	Ac103341 Human mic
C 455	11.4	60.0	24	10	ADC63611	Adc63611 Human PRO	C 528	11.4	60.0	25	9	ACI11367	Ac111367 Human mic
C 456	11.4	60.0	24	10	ADC66711	Adc66711 Human PRO	C 529	11.4	60.0	25	10	ACA05215	Aca05215 M. tuberc

c 530	11.4	60.0	25	12	ADH72891	Adh72891 M. tuberc	603	11.2	58.9	19	14	ABE55223	Aee55223 Human hai
531	11.4	60.0	25	12	ADP14600	Renal cel	604	11.2	58.9	19	14	ABE55219	Aee55219 Human hai
c 532	11.4	60.0	25	13	ADR42656	Acetylase	c 605	11.2	58.9	19	14	ABE55224	Aee55224 Human hai
533	11.4	60.0	25	13	ADR56507	Drug ther	c 606	11.2	58.9	19	15	ABE65108	Aee65108 Human vit
534	11.4	60.0	26	2	AAV65661	Adenoviru	607	11.2	58.9	19	15	ABE65364	Aee65364 Human vit
535	11.4	60.0	26	2	AAV57191	Porcine O	608	11.2	58.9	20	2	AAQ73373	AaQ73373 Anti-HSV-
c 536	11.4	60.0	26	3	AAV58311	Human PRO	609	11.2	58.9	20	2	AAQ61986	AAQ61986 Inosine-s
537	11.4	60.0	26	13	ADU87192	B melanom	610	11.2	58.9	20	2	AAQ86840	AAQ86840 Antisense
c 538	11.4	60.0	26	14	ABE98383	Rat GLUT3	611	11.2	58.9	20	2	AAAT48971	AAAT48971 Complem
c 539	11.4	60.0	26	14	ASEC62733	Human 36B	612	11.2	58.9	20	2	AAAT48972	AAAT48972 Complem
540	11.4	60.0	27	8	ABV73361	Insect ce	c 613	11.2	58.9	20	2	ADG77677	ADG77677 Canine di
541	11.4	60.0	27	10	AAAL56130	EPO-Fc ex	614	11.2	58.9	20	2	AAV53590	AAV53590 Nucleotid
542	11.4	60.0	27	12	ADU010527	Human EPO	615	11.2	58.9	20	2	AAZ03860	AAZ03860 PCR prime
543	11.4	60.0	27	12	ADP03174	Allele sp	c 616	11.2	58.9	20	3	AAA40892	AAA40892 Murine TN
544	11.4	60.0	27	14	ADV97101	PCR prime	c 617	11.2	58.9	20	3	AAZ74856	AAZ74856 Human bia
545	11.4	60.0	28	2	AAV31811	Nucleotid	c 618	11.2	58.9	20	4	AAF59863	AAF59863 Human pro
546	11.4	60.0	28	2	AAZ230722	PCR prime	619	11.2	58.9	20	6	ABL58945	ABL58945 Human tum
547	11.4	60.0	28	3	AAZ60288	Primer 7	c 620	11.2	58.9	20	9	ABZ771041	ABZ771041 Human HXR
548	11.4	60.0	28	6	ABA93428	Aspergill	c 621	11.2	58.9	20	9	ACD05120	ACD05120 Tumour ne
549	11.4	60.0	28	13	ADT62023	Vector ps	c 622	11.2	58.9	20	10	ABZ87613	ABZ87613 Human oli
550	11.4	60.0	29	3	AAA04352	Polymorph	c 623	11.2	58.9	20	11	ABD23843	ABD23843 Human myo
551	11.4	60.0	29	4	AAAS09212	PCR prime	c 624	11.2	58.9	20	12	ADK95473	ADK95473 Primer of
552	11.4	60.0	29	6	ADT27411	Murine er	c 625	11.2	58.9	20	12	ADL57961	ADL57961 Human ESM
553	11.4	60.0	29	10	ADC15541	Mouse ery	c 626	11.2	58.9	20	12	ADL58177	ADL58177 Human ESM
554	11.4	60.0	29	11	ADM33836	Human ery	c 627	11.2	58.9	20	12	ADL57919	ADL57919 Human ESM
555	11.4	60.0	29	13	ADR48967	Human EPO	c 628	11.2	58.9	20	12	ADL57893	ADL57893 Human ESM
556	11.4	60.0	29	13	ADW47499	Human EPO	c 629	11.2	58.9	20	12	ADL57899	ADL57899 Human ESM
557	11.4	60.0	29	14	AEA18916	HuEPO-L-v	c 630	11.2	58.9	20	12	ADO31326	ADO31326 Human XT-
558	11.4	60.0	29	14	AEA88736	Human ery	c 631	11.2	58.9	20	12	ADQ29202	ADQ29202 Mouse TNF
559	11.4	60.0	29	15	AEF69792	Human L-P	c 632	11.2	58.9	20	13	ADR02718	ADR02718 Antisense
c 560	11.4	60.0	30	15	AEF69791	Human L-P	c 633	11.2	58.9	20	14	ADW96343	ADW96343 CRX PCR p
561	11.4	60.0	30	5	AAF84064	5' and 3'	c 634	11.2	58.9	20	14	ADW38591	ADW38591 Hot flash
c 562	11.4	60.0	30	10	ADH34370	Human t-P	c 635	11.2	58.9	20	14	ADY60155	ADY60155 Antisense
c 563	11.4	60.0	30	14	ADZ36927	Rice ZnCe	c 636	11.2	58.9	20	14	ADZ84800	ADZ84800 Murine so
564	11.4	60.0	30	15	AEF00111	DNA probe	c 637	11.2	58.9	21	2	AAV67434	AAV67434 Nucleotid
c 565	11.2	58.9	15	8	ABZ69100	Fragment	c 638	11.2	58.9	21	2	AAZ26088	AAZ26088 Human pol
c 566	11.2	58.9	15	10	ADF29171	Beta-glob	c 639	11.2	58.9	21	2	AAK09042	AAK09042 Tumour ne
c 567	11.2	58.9	16	3	AAA48865	Reverse p	640	11.2	58.9	21	4	AAF95481	AAF95481 Human gen
c 568	11.2	58.9	17	8	ABT35415	Tumour su	641	11.2	58.9	21	4	AAH00829	AAH00829 Trypanoso
c 569	11.2	58.9	17	8	ACA06653	NFKB sub-	c 642	11.2	58.9	21	6	ABS98383	ABS98383 Human mul
570	11.2	58.9	17	8	ABZ61913	Human H-R	c 643	11.2	58.9	21	6	ABN85352	ABN85352 ds-protei
c 571	11.2	58.9	17	8	ABZ62012	Human H-R	c 644	11.2	58.9	21	10	ABZ80350	ABZ80350 Human Emx
c 572	11.2	58.9	17	8	ACC65130	Murine ol	c 645	11.2	58.9	21	12	ADP03287	ADP03287 PCR prime
573	11.2	58.9	17	10	ADF62816	Human PCC	c 646	11.2	58.9	21	12	ADP03287	ADP03287 PCR prime
574	11.2	58.9	17	10	ADF62818	Human PCC	c 647	11.2	58.9	21	13	AEA97450	AEA97450 Human lup
575	11.2	58.9	17	11	ADL50606	Human PCR	648	11.2	58.9	21	14	ADV65744	ADV65744 Sense str
576	11.2	58.9	17	14	ADY67792	Autism ge	649	11.2	58.9	21	14	ADX45158	ADX45158 DNA probe
577	11.2	58.9	17	14	ADZ30987	Human H-R	650	11.2	58.9	21	14	ADX45158	ADX45158 DNA probe
c 578	11.2	58.9	17	14	ADZ31086	Human H-R	651	11.2	58.9	22	2	AAV68315	AAV68315 Loci-spec
c 579	11.2	58.9	18	8	ABZ76727	Cytotplasm	652	11.2	58.9	22	2	AAV42511	AAV42511 PCR prime
c 580	11.2	58.9	18	10	ADG89466	Human mat	653	11.2	58.9	22	2	AAV42495	AAV42495 PCR prime
581	11.2	58.9	18	11	ADL61707	Human p16	654	11.2	58.9	22	2	AAV42481	AAV42481 PCR prime
c 582	11.2	58.9	18	11	ADM92691	SNP-conta	c 655	11.2	58.9	22	3	AAZ29172	AAZ29172 Primer 10
c 583	11.2	58.9	18	14	AEC51557	Antisense	c 656	11.2	58.9	22	3	AAZ93863	AAZ93863 Primer us
c 584	11.2	58.9	18	14	AEC53955	Antisense	c 657	11.2	58.9	22	8	ACF03723	ACF03723 PCR prime
c 585	11.2	58.9	18	14	AEC51584	Antisense	658	11.2	58.9	22	13	ADR03452	ADR03452 PCR prime
c 586	11.2	58.9	18	14	AEF31359	Cotton AR	c 659	11.2	58.9	22	14	ADV45283	ADV45283 Human Cpg
587	11.2	58.9	19	2	AAV47454	Foldback	c 660	11.2	58.9	22	14	ADV46033	ADV46033 Human Cpg
588	11.2	58.9	19	2	AAV93945	Primer RS	661	11.2	58.9	23	3	AA301048	AA301048 PCR prime
589	11.2	58.9	19	10	ADF54291	Human GAB	662	11.2	58.9	23	4	AAI65547	AAI65547 Primer fo
c 590	11.2	58.9	19	10	ADF53955	Human GAB	663	11.2	58.9	23	4	AAI65547	AAI65547 Primer fo
c 591	11.2	58.9	19	10	ADG34896	Human TNF	664	11.2	58.9	23	6	ADJ42937	ADJ42937 Human PLA
592	11.2	58.9	19	10	ADG35019	Human TNF	665	11.2	58.9	23	12	ADJ62187	ADJ62187 Human 143
593	11.2	58.9	19	14	ADZ85485	Methylati	666	11.2	58.9	24	2	AAQ28855	AAQ28855 Probe Ol-
594	11.2	58.9	19	14	AEC33540	Human GAB	c 667	11.2	58.9	24	2	AAQ99684	AAQ99684 Homology
c 595	11.2	58.9	19	14	AEC33204	Human GAB	c 668	11.2	58.9	24	2	ADH29722	ADH29722 Human IL-
596	11.2	58.9	19	14	AED44268	Human TNF	669	11.2	58.9	24	2	AAAT58454	AAAT58454 Granulocy
c 597	11.2	58.9	19	14	AED44145	Human TNF	670	11.2	58.9	24	2	AAAT91911	AAAT91911 Granulocy
c 598	11.2	58.9	19	14	ABE55222	Human hai	c 671	11.2	58.9	24	2	AAV56297	AAV56297 Human BRC
c 599	11.2	58.9	19	14	ABE55220	Human hai	c 672	11.2	58.9	24	2	AAV62234	AAV62234 PCR prime
600	11.2	58.9	19	14	ABE55221	Human hai	c 673	11.2	58.9	24	2	AAV32090	AAV32090 BRCA1 gen
c 601	11.2	58.9	19	14	ABE55218	Human hai	674	11.2	58.9	24	2	AAV55763	AAV55763 Probe Ol-
602	11.2	58.9	19	14	ABE55225	Human hai	675	11.2	58.9	24	2	AAV82564	AAV82564 Probe Ol-

676	11.2	58.9	24	3	AAC68613	Aac68613 Human G-C	749	11	57.9	11	6	AAL47358	Aa147358 Human NMD
c 677	11.2	58.9	24	3	AAC60811	Aac60811 Human BRC	750	11	57.9	11	8	ABX77662	Abx77662 Human N-m
c 678	11.2	58.9	24	4	AAS07427	Aas07427 PCR prime	751	11	57.9	11	9	ACD98327	Ac98327 Human NMD
c 679	11.2	58.9	24	4	ABL51702	Ab151702 Human GFR	752	11	57.9	11	10	AAD59659	Aad59659 Human NMD
c 680	11.2	58.9	24	6	ABS72032	Ab572032 Human GFR	753	11	57.9	11	10	ABX98517	Abx98517 Human N-m
c 681	11.2	58.9	24	8	ABV75838	Abv75838 CD81 fwd	754	11	57.9	11	10	ABX92866	Abx92866 Human N-m
c 682	11.2	58.9	24	9	ADA45330	Ada45330 Human GTP	755	11	57.9	11	12	ADQ35259	Adq35259 Human hai
c 683	11.2	58.9	24	9	ADA45330	Ada45330 Human BRC	756	11	57.9	11	12	AAI14874	Aai14874 Triple he
c 684	11.2	58.9	24	10	ADC63308	Adc63308 Human BRC	757	11	57.9	11	13	AAX14866	Aax14866 Triple he
c 685	11.2	58.9	24	10	ADL01902	Adl01902 Human gra	758	11	57.9	11	13	AAX14866	Aax14866 Triple he
c 686	11.2	58.9	24	11	ADM13669	Adm13669 Oligonuc1	759	11	57.9	11	13	ABC72338	Abc72338 Oligonuc1
c 687	11.2	58.9	24	12	ADM86702	Adm86702 Human G-C	c 760	11	57.9	11	13	ABF86424	Abf86424 Oligonuc1
c 688	11.2	58.9	24	12	ADMI2802	Admi2802 Single mu	c 761	11	57.9	11	13	ABF86425	Abf86425 Oligonuc1
c 689	11.2	58.9	24	12	ADP98368	Adp98368 C. albica	c 762	11	57.9	11	15	ABC72339	Abc72339 Oligonuc1
c 690	11.2	58.9	25	2	AQ76083	Aeq76083 HSV tk ge	c 763	11	57.9	11	17	AAI67334	Aai67334 Human FKB
c 691	11.2	58.9	25	4	AH78306	Aah78306 PCR prime	c 764	11	57.9	11	3	AAF06237	Aaf06237 Hammerhea
c 692	11.2	58.9	25	6	ABZ21959	Abz21959 Human Apo	765	11	57.9	11	14	AEC25957	Aec25957 Human all
c 693	11.2	58.9	25	6	ABL91161	Ab191161 Hominidae	766	11	57.9	11	14	AEC28323	Aec28323 Human all
c 694	11.2	58.9	25	6	ABA98501	Ab98501 TNFalpha	c 767	11	57.9	11	19	AAQ38084	Aaq38084 PCR prime
c 695	11.2	58.9	25	9	ACI66902	Aci66902 Human mic	c 768	11	57.9	11	19	AAQ05453	Aaq05453 Primer 1
c 696	11.2	58.9	25	9	ACI25049	Aci25049 Human mic	c 769	11	57.9	11	19	AAQ03083	Aaq03083 p53 expre
c 697	11.2	58.9	25	9	ACI73934	Aci73934 Human mic	c 770	11	57.9	11	19	AAQ90801	Aaq90801 Human C-C
c 698	11.2	58.9	25	10	ADF63559	Adf63559 Human PCC	c 771	11	57.9	11	19	AEa42854	Aee42854 Human hai
c 699	11.2	58.9	25	10	ADF63569	Adf63569 Human PCC	c 772	11	57.9	11	19	AEa42853	Aee42853 Human hai
c 700	11.2	58.9	25	14	ADZ28193	Adz28193 Neo gene	c 773	11	57.9	11	19	AEf36779	Aef36779 Human SDF
c 701	11.2	58.9	25	15	AEe66295	Aee66295 Small int	c 774	11	57.9	11	20	AAA40890	Aaa40890 Murine TN
c 702	11.2	58.9	26	2	AX40765	Aax40765 Oligonuc1	c 775	11	57.9	11	20	AAF23215	Aaf23215 Oligonuc1
c 703	11.2	58.9	26	2	AX40797	Aax40797 Oligonuc1	c 776	11	57.9	11	20	AAQ08862	Aaq08862 Human PD-
c 704	11.2	58.9	26	3	AAA10506	Aaa10506 PCR prime	c 777	11	57.9	11	20	AAQ08771	Aaq08771 Human PD-
c 705	11.2	58.9	26	4	AD13137	Ad13137 Human MTS	c 778	11	57.9	11	20	ABA83463	Ab83463 Human MP-
c 706	11.2	58.9	26	5	AF62520	Af62520 Primer #1	c 779	11	57.9	11	20	ABA83462	Ab83462 Human MP-
c 707	11.2	58.9	26	6	ABK66444	Abk66444 Human gen	c 780	11	57.9	11	20	AA46510	Aa46510 Human glu
c 708	11.2	58.9	26	10	ADC10394	Adc10394 Human NOV	c 781	11	57.9	11	20	ACD05118	Acd05118 Tumour ne
c 709	11.2	58.9	26	13	ADZ15701	Adz15701 Mutagenic	c 782	11	57.9	11	20	ADD20688	Add20688 Oreochrom
c 710	11.2	58.9	26	13	ADZ15702	Adz15702 Mutagenic	c 783	11	57.9	11	20	ADD69530	Add69530 Food enri
c 711	11.2	58.9	26	14	ABE98375	Ab98375 Rat GFAP	c 784	11	57.9	11	20	ADH76945	Adh76945 Lac Z A P
c 712	11.2	58.9	26	14	ABE90638	Ab90638 Rat GFAP	c 785	11	57.9	11	20	ABZ98854	Abz98854 Human PDE
c 713	11.2	58.9	26	14	ABE98412	Ab98412 Rat GFAP	c 786	11	57.9	11	20	ABZ93512	Abz93512 Human oli
c 714	11.2	58.9	26	14	ABE94256	Ab94256 Rat GFAP	c 787	11	57.9	11	20	ADM64961	Adm64961 NRY polym
c 715	11.2	58.9	26	14	ABE98678	Ab98678 Rat GFAP	c 788	11	57.9	11	20	ABD31885	Abd31885 Human PDE
c 716	11.2	58.9	26	14	ABE79133	Ab79133 Rat GFAP	c 789	11	57.9	11	20	ABD29742	Abd29742 Aa626698-
c 717	11.2	58.9	27	2	AA735053	Aat35053 HSV thymi	c 790	11	57.9	11	20	ADJ60737	Adj60737 Oligonuc1
c 718	11.2	58.9	27	2	AAZ23809	Aaz23809 Mouse Kv6	c 791	11	57.9	11	20	ADQ46226	Adq46226 Human oli
c 719	11.2	58.9	27	2	AAZ83866	Aaz83866 Human lig	c 792	11	57.9	11	20	ADQ47461	Adq47461 S parvulu
c 720	11.2	58.9	27	4	AAH43365	Aah43365 KC (sense)	c 793	11	57.9	11	20	ADQ29200	Adq29200 Mouse TNF
c 721	11.2	58.9	27	4	AAH43365	Aah43365 KC (sense)	c 794	11	57.9	11	20	ADQ2716	Adq2716 Antisense
c 722	11.2	58.9	27	4	AAH43365	Aah43365 KC (sense)	c 795	11	57.9	11	20	ADQ29200	Adq29200 Mouse TNF
c 723	11.2	58.9	27	5	AAF27956	Aaf27956 PCR prime	c 796	11	57.9	11	20	ADQ2716	Adq2716 Antisense
c 724	11.2	58.9	27	6	ABK14711	Abk14711 PCR prime	c 797	11	57.9	11	20	ADY59632	Ady59632 C. utilis
c 725	11.2	58.9	27	14	AEA35032	Aea35032 Hb9 enhan	c 798	11	57.9	11	20	ADY60153	Ady60153 Antisense
c 726	11.2	58.9	28	4	ADQ2151	Adq2151 P. funicu	c 799	11	57.9	11	20	AEb95081	Aeb95081 Mouse eIF
c 727	11.2	58.9	28	6	ADQ35051	Adq35051 C. glutan	c 800	11	57.9	11	20	AEb94890	Aeb94890 Mouse eIF
c 728	11.2	58.9	28	9	ACC85468	Acc85468 T thermoh	c 801	11	57.9	11	20	AEC27442	Aec27442 Human all
c 729	11.2	58.9	28	13	ADW75898	Adw75898 Novel tra	c 802	11	57.9	11	21	AAX28531	Aax28531 Oligonuc1
c 730	11.2	58.9	28	14	ADZ05923	Adz05923 Probe use	c 803	11	57.9	11	21	AAQ07261	Aaq07261 Primer fo
c 731	11.2	58.9	28	14	ABE02885	Aeb02885 Gene chip	c 804	11	57.9	11	21	AAQ07261	Aaq07261 Primer fo
c 732	11.2	58.9	29	6	ABK49839	Abk49839 Mychis ta	c 805	11	57.9	11	21	AAQ07261	Aaq07261 Primer fo
c 733	11.2	58.9	29	8	ADW72303	Adw72303 Rice gene	c 806	11	57.9	11	21	AAQ07261	Aaq07261 Primer fo
c 734	11.2	58.9	29	14	ADX45157	Adx45157 DNA probe	c 807	11	57.9	11	21	AAQ07261	Aaq07261 Primer fo
c 735	11.2	58.9	30	2	AAQ93302	Aaq93302 Two membe	c 808	11	57.9	11	21	AAQ07261	Aaq07261 Primer fo
c 736	11.2	58.9	30	2	AAQ10602	Aaq10602 CSF clone	c 809	11	57.9	11	21	AAQ07261	Aaq07261 Primer fo
c 737	11.2	58.9	30	2	AAQ66310	Aaq66310 Oligonuc1	c 810	11	57.9	11	21	AAQ07261	Aaq07261 Primer fo
c 738	11.2	58.9	30	4	AAQ70583	Aaq70583 2'NH2 RNA	c 811	11	57.9	11	21	ACC83441	Acc83441 PROC hypo
c 739	11.2	58.9	30	10	ADF43460	Adf43460 PCR prime	c 812	11	57.9	11	21	ADH16986	Adh16986 Human mtD
c 740	11.2	58.9	30	12	ADI28878	Adi28878 Human ser	c 813	11	57.9	11	21	ADU13100	Adj13100 Human DNA
c 741	11.2	58.9	30	12	ADO56474	Ado56474 Human cyc	c 814	11	57.9	11	21	ADU14315	Adj14315 DNA relat
c 742	11.2	58.9	30	12	ADP46371	Adp46371 PCR prime	c 815	11	57.9	11	21	ADQ92427	Adq92427 5-alpha r
c 743	11.2	58.9	30	14	ADM42937	Adm42937 Forward p	c 816	11	57.9	11	21	ADQ93717	Adq93717 3-beta-hy
c 744	11.2	58.9	30	15	AEF07299	Aef07299 SPVUE SNP	c 817	11	57.9	11	21	ADQ93536	Adq93536 3-beta-hy
c 745	11	57.9	11	2	AAQ79374	Aaq79374 Human NMD	c 818	11	57.9	11	21	ADR18381	Adr18381 Human GOB
c 746	11	57.9	11	2	AAV82891	Aav82891 InSert pr	c 819	11	57.9	11	21	ADR18469	Adr18469 Human GOB
c 747	11	57.9	11	3	AAZ38705	Aaz38705 Human NMD	c 820	11	57.9	11	21	ADW72549	Adw72549 Mitochond
c 748	11	57.9	11	6	ABI99171	Abi99171 Human NMD	c 821	11	57.9	11	21	ADW72547	Adw72547 Mitochond

822	11	57.9	21	14	ADW72548	Adw72548 Mitochond	895	11	57.9	27	6	ABK53065	Abk53065 S. Cerevi
c 823	11	57.9	21	14	AEC65320	Aec65320 DNA for s	896	11	57.9	27	7	ADI93703	Adi93703 Murine IL
c 824	11	57.9	21	14	AEb99780	AEb99780 DNA encod	897	11	57.9	27	7	ADI94659	Adi94659 FRET olig
825	11	57.9	21	15	AE28389	Ae28389 Escherich	c 898	11	57.9	27	8	ABV72381	Abv72381 PCR prime
826	11	57.9	21	15	AEF02561	Aef02561 Escherich	c 899	11	57.9	27	10	ADG38359	Adg38359 Anti-HIV
c 827	11	57.9	22	2	AAQ95239	AAq95239 Simple ta	900	11	57.9	27	10	ABZ95568	Abz95568 Human end
828	11	57.9	22	4	AAQ52229	AAq52229 ICE/lacZ	901	11	57.9	27	11	ABD19718	Abd19718 Human end
c 829	11	57.9	22	4	AAEF24806	AAef24806 PCR prime	902	11	57.9	27	13	ADT77699	Adt77699 Neisseria
c 830	11	57.9	22	4	AAF322208	AAf322208 Arabidops	903	11	57.9	27	13	ADY27216	Ady27216 Human CX
c 831	11	57.9	22	10	ADD19577	AdD19577 Oreochrom	c 904	11	57.9	27	13	ADZ47977	Adz47977 DESCL1 rel
c 832	11	57.9	22	11	ADZ09135	Adz09135 Novel DNA	905	11	57.9	27	14	AEC07377	Aec07377 Herpes vi
c 833	11	57.9	22	12	ADI28447	Adi28447 Arabidops	c 906	11	57.9	27	14	AEC07384	Aec07384 Herpes vi
834	11	57.9	23	2	AAAX59051	AAx59051 Human tra	907	11	57.9	28	2	AAZ22980	Aaz22980 Canine BP
c 835	11	57.9	23	3	AAAC66148	AAc66148 21-hydrox	c 908	11	57.9	28	5	AAF58388	Aaf58388 Murine GM
c 836	11	57.9	23	3	AAAC66152	AAc66152 21-hydrox	909	11	57.9	28	10	ADF39553	Adf39553 SFRP5 gen
c 837	11	57.9	23	3	AAAC66152	AAc66152 21-hydrox	910	11	57.9	28	12	ADN36198	Adn36198 Probe #27
c 838	11	57.9	23	14	ADV45600	Adv45600 Human CpG	911	11	57.9	28	12	ADN36201	Adn36201 Probe #28
839	11	57.9	23	15	AEF21532	Aef21532 Human non	912	11	57.9	28	12	ADN36193	Adn36193 Probe #27
c 840	11	57.9	24	6	AAAS16482	AAa16482 Rat (Na,K	913	11	57.9	28	12	ADN36195	Adn36195 Probe #27
c 841	11	57.9	24	10	ADD335579	AdD335579 Escherich	914	11	57.9	28	12	ADN36194	Adn36194 Probe #27
c 842	11	57.9	24	10	ACH00666	Ach00666 Mammalian	915	11	57.9	28	12	ADN36200	Adn36200 Probe #28
c 843	11	57.9	24	10	ADF79194	Adf79194 PSA PCR p	916	11	57.9	28	12	ADN36199	Adn36199 Probe #28
c 844	11	57.9	24	13	ADT62653	Adt62653 Genetic p	917	11	57.9	28	12	ADN36202	Adn36202 Probe #28
c 845	11	57.9	24	13	ADV34197	Adv34197 Improved	918	11	57.9	28	12	ADN36196	Adn36196 Probe #27
c 846	11	57.9	24	14	ADZ44637	Adz44637 PCR prime	919	11	57.9	28	12	ADN36197	Adn36197 Probe #27
c 847	11	57.9	25	2	AAQ20094	AAq20094 Cytomegal	920	11	57.9	29	3	AAA04353	Aaa04353 Polymorph
c 848	11	57.9	25	2	AAQ58565	AAq58565 CMV MIE g	921	11	57.9	29	3	AAA04167	Aaa04167 Polymorph
c 849	11	57.9	25	2	AAAX28532	AAx28532 Oligonuc	922	11	57.9	29	3	AAZ34541	Aaz34541 DNA seque
c 850	11	57.9	25	2	AAQ76059	AAq76059 hCMV Prim	923	11	57.9	29	3	AAZ34542	Aaz34542 DNA seque
c 851	11	57.9	25	2	AAQ65567	AAq65567 Oligonuc	c 924	11	57.9	29	5	AAH45090	Aah45090 Murine in
c 852	11	57.9	25	2	AAV07715	AAv07715 Cytomegal	925	11	57.9	29	10	ADA01460	Ada01460 Mouse ang
c 853	11	57.9	25	2	AAAX91197	AAx91197 CMV immed	c 926	11	57.9	29	12	ADN94975	Adn94975 Rat fatty
c 854	11	57.9	25	2	AAAX59073	AAx59073 CMV detec	c 927	11	57.9	29	14	ADX70075	Adx70075 Mouse p16
c 855	11	57.9	25	3	AAAX82992	AAx82992 CMV detec	928	11	57.9	30	2	AAAT89034	Aat89034 Solid pha
c 856	11	57.9	25	3	AAZ59161	AAz59161 Primer #2	c 929	11	57.9	30	2	AAZ30102	Aaz30102 PCR prime
c 857	11	57.9	25	4	AAH21680	Aah21680 Human cyt	c 930	11	57.9	30	2	AAZ28083	Aaz28083 Murine IL
c 858	11	57.9	25	4	AAH21688	Aah21688 Human cyt	c 931	11	57.9	30	4	AAAS95132	Aas95132 Otoferrin
c 859	11	57.9	25	4	AAH21689	Aah21689 Human int	c 932	11	57.9	30	5	AAAF58386	Aaf58386 Murine IL
c 860	11	57.9	25	6	ABX00061	Abx00061 Human int	c 933	11	57.9	30	6	ABA99121	Ab99121 Sense pri
861	11	57.9	25	6	ABK70483	Abk70483 In-situ a	c 934	11	57.9	30	6	AAAL49448	Aal49448 High thro
c 862	11	57.9	25	9	ACI28450	ACi28450 Human mic	935	11	57.9	30	7	ADI93711	Adi93711 Murine IL
c 863	11	57.9	25	9	ACI60867	ACi60867 Human mic	936	11	57.9	30	7	ADI93717	Adi93717 Murine IL
c 864	11	57.9	25	9	ACI67700	ACi67700 Human mic	c 937	11	57.9	30	7	ADI93872	Adi93872 Human IL
c 865	11	57.9	25	9	ACI73108	ACi73108 Human mic	c 938	11	57.9	30	10	ADA242609	Ada242609 Human inf
c 866	11	57.9	25	9	ACI41114	ACi41114 Human mic	c 939	11	57.9	30	12	ADP08610	Adp08610 PCR prime
c 867	11	57.9	25	9	ACH51542	ACH51542 DNA targe	c 940	11	57.9	30	14	AED11717	Aed11717 Endonucle
c 868	11	57.9	25	9	ACH51543	ACH51543 DNA targe	c 941	11	57.9	30	14	AED19711	Aed19711 Human CMP
c 869	11	57.9	25	11	ADL59803	ADl59803 Arabidops	c 942	11	57.9	30	14	AEQ01874	Aeq01874 Restricti
c 870	11	57.9	25	12	ADJ14316	ADj14316 DNA relat	c 943	11	57.9	30	14	AEQ01876	Aeq01876 Restricti
c 871	11	57.9	25	13	ADRI15565	ADr15565 Mouse flo	c 944	11	57.9	30	15	AEF07567	Aef07567 PFTK1 SNP
c 872	11	57.9	25	14	ADY81843	ADy81843 Thale-cre	c 945	10.8	56.8	14	2	ADG14093	Adg14093 Porcine r
c 873	11	57.9	25	14	AED65866	Aed65866 Arabidops	c 946	10.8	56.8	15	4	AAAS04330	Aas04330 Human DAC
c 874	11	57.9	25	14	AED65541	Aed65541 Arabidops	c 947	10.8	56.8	15	10	ADF83518	Adf83518 Human MC1
c 875	11	57.9	25	14	AED80192	Aed80192 Arabidops	c 948	10.8	56.8	15	12	ADH70514	Adh70514 Human Vbe
c 876	11	57.9	25	15	ABEE5038	ABee5038 Human TGF	c 949	10.8	56.8	16	15	ADH70478	Adh70478 Human Vbe
c 877	11	57.9	25	15	ABEE27028	ABee27028 Arabidops	c 950	10.8	56.8	16	15	AAAS15521	Aas15521 N-acetyl
c 878	11	57.9	26	2	AAQ04998	AAq04998 Sequence	951	10.8	56.8	16	16	AAI68609	Aai68609 ICAM-1 tr
c 879	11	57.9	26	2	AAQ33261	AAq33261 Triplex f	952	10.8	56.8	16	14	ADW01656	Adw01656 DNA oligo
c 880	11	57.9	26	2	AAQ36286	AAq36286 EGFR2par	c 953	10.8	56.8	16	14	ADW01656	Adw01656 VEGF RNA
c 881	11	57.9	26	2	AAQ36287	AAq36287 EGFR2anti	c 954	10.8	56.8	16	14	ADW01656	Adw01656 Human c-m
c 882	11	57.9	26	2	AAQ40790	AAq40790 Oligonuc	c 955	10.8	56.8	17	2	AAAX63959	Aax63959 Rabbit st
c 883	11	57.9	26	2	AAAX40756	AAx40756 Oligonuc	c 956	10.8	56.8	17	3	AAAF07059	Aaf07059 Hammerhea
c 884	11	57.9	26	3	AAAX96685	AAx96685 PCR prime	c 957	10.8	56.8	17	3	AAAC73558	Aac73558 Reverse p
c 885	11	57.9	26	5	AAAF17119	AAf17119 Informati	c 958	10.8	56.8	17	4	ABK00896	Abk00896 Human NOG
c 886	11	57.9	26	13	ADR32549	Adr32549 Human nic	c 959	10.8	56.8	17	4	ABK00897	Abk00897 Human NOG
c 887	11	57.9	26	13	ADR15564	Adr15564 Mouse flo	c 960	10.8	56.8	17	4	ABK00899	Abk00899 Human NOG
c 888	11	57.9	27	2	AAAT51632	AAt51632 Viral int	c 961	10.8	56.8	17	4	ABK00898	Abk00898 Human NOG
c 889	11	57.9	27	2	AAAT76517	AAt76517 Endotheli	c 962	10.8	56.8	17	5	ADV03317	Adv03317 Human BAC
c 890	11	57.9	27	2	AAAX79221	AAx79221 Oligonuc	c 963	10.8	56.8	17	5	ADV47057	Adv47057 HBV inozy
c 891	11	57.9	27	3	AAAX54308	Aax54308 Endotheli	c 964	10.8	56.8	17	5	ADV46409	Adv46409 Human Her
c 892	11	57.9	27	3	AAAO9371	AAa09371 Primer B	c 965	10.8	56.8	17	5	ADV47056	Adv47056 HBV inozy
c 893	11	57.9	27	3	AAAX3752	AAa33752 Low adeno	c 966	10.8	56.8	17	5	ADV47972	Adv47972 HBV G-cle
c 894	11	57.9	27	5	AAAS04265	AAa04265 Saccharom	c 967	10.8	56.8	17	5	ADV61258	Adv61258 HBV amber

c 968 10.8 56.8 17 5 ADV48340
c 969 10.8 56.8 17 5 ADV49040
c 970 10.8 56.8 17 6 ABN02323
c 971 10.8 56.8 17 6 ABN02322
c 972 10.8 56.8 17 6 ABN02320
c 973 10.8 56.8 17 6 ABN02321
c 974 10.8 56.8 17 6 ABN06801
c 975 10.8 56.8 17 6 ABN06797
c 976 10.8 56.8 17 6 ABS98503
c 977 10.8 56.8 17 6 ACN11587
c 978 10.8 56.8 17 6 ACN03787
c 979 10.8 56.8 17 6 ACN04889
c 980 10.8 56.8 17 6 ACN05903
c 981 10.8 56.8 17 6 ACN11588
c 982 10.8 56.8 17 6 ABT36139
c 983 10.8 56.8 17 8 ACA09149
c 984 10.8 56.8 17 8 ACA09148
c 985 10.8 56.8 17 8 ACA09148
c 986 10.8 56.8 17 8 ABZ60669
c 987 10.8 56.8 17 8 ABZ65426
c 988 10.8 56.8 17 8 ABZ65427
c 989 10.8 56.8 17 8 ACD53277
c 990 10.8 56.8 17 8 ACD53278
c 991 10.8 56.8 17 8 ACD53277
c 992 10.8 56.8 17 8 ACC66572
c 993 10.8 56.8 17 10 ADB41031
c 994 10.8 56.8 17 12 ADM58921
c 995 10.8 56.8 17 12 ADM59380
c 996 10.8 56.8 17 12 ADM58922
c 997 10.8 56.8 17 13 ACN69891
c 998 10.8 56.8 17 13 ACN69887
c 999 10.8 56.8 17 13 ACN65410
c1000 10.8 56.8 17 13 ACN65411

ALIGNMENTS

RESULT 1
ADF17589
ID ADF17589 standard; DNA; 22 BP.
XX
AC ADF17589;
AC
DT 12-FEB-2004 (first entry)
XX
DE Beta A PCR primer SEQ ID NO:1.
XX
KW neovascularisation agent; activin stimulator;
KW anti-neovascularisation agent; activin inhibitor;
KW neovascularisation regulator; ischaemic condition; atherosclerosis;
KW occlusive arteriosclerosis; lower limb vascular occlusion;
KW myocardial infarction; angina pectoris; cerebral embolism;
KW recalcitrant skin ulcer; diabetes; pancreatic islet cell regeneration;
KW diabetic retinopathy; senile macular degeneration;
KW chronic rheumatoid arthritis; cancer; psoriasis vulgaris; PCR primer;
KW beta A; ss.
XX
OS Synthetic.
XX
PN WO2003094966-A1.
XX
PD 20-NOV-2003.
XX
PF 12-MAY-2003; 2003WO-JP005901.
XX
PR 10-MAY-2002; 2002JP-00135575.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Kojima I, Maeshima K, Eto Y;
XX
DR WPI; 2003-903943/82.

XX Agents promoting or suppressing neovascularization containing activin
PT stimulator or activin inhibitor, to treat ischemic conditions, diabetes
PT and skin ulcers, or rheumatoid arthritis, diabetic retinopathy and
PT cancer, etc.
XX
PS Example 2; SEQ ID NO 1; 37pp; Japanese.
XX
CC The present invention describes a neovascularisation agent (I), which has
CC an activin stimulator as an active component. Also described: (1) an anti
CC -neovascularisation agent (II) containing an activin inhibitor as an
CC active component; and (2) a neovascularisation regulator comprising (I)
CC and (II). The neovascularisation agent (I) can be used to prevent or
CC treat ischaemic conditions, atherosclerosis, occlusive arteriosclerosis,
CC lower limb vascular occlusion, myocardial infarction, angina pectoris,
CC cerebral embolism, recalcitrant skin ulcers; and diabetes, through
CC pancreatic islet cell regeneration. The anti-neovascularisation agent
CC (II) can be used to prevent or treat diabetic retinopathy, senile macular
CC degeneration, chronic rheumatoid arthritis, cancer, psoriasis vulgaris.
CC The present sequence represents a PCR primer for beta A, which is used in
CC an example from the present invention.
XX
SQ Sequence 22 BP; 5 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 77.9%; Score 14.8; DB 10; Length 22;
Best Local Similarity 88.9%; Pred. No. 8.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGAGAGGGGTGGTGC 18
Db 5 GGAGAGGGGTGGTGC 22
RESULT 2
ABX10197
ID ABX10197 standard; DNA; 26 BP.
XX
AC ABX10197;
XX
DT 27-JAN-2003 (first entry)
XX
DE S. aggregatum Delta4-desaturase PCR primer RO1239.
XX
KW ss; PCR; primer; delta4-desaturase; polyunsaturated fatty acid; PUFA;
KW nutritional; cosmetic; pharmaceutical; animal feed;
KW omega6-docosapentaenoic acid; docosahexaenoic acid; restenosis;
KW angioplasty; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW osteoporosis; kidney stone; urinary tract stone; cancer; cachexia;
KW cancer; diabetes; eczema; gastrointestinal bleeding; endometriosis;
KW premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue;
KW viral infections; acquired immunodeficiency syndrome; AIDS;
KW multiple sclerosis; inflammatory skin disorder; blood pressure;
KW platelet aggregation; vasodilation; cholesterol level.
XX
OS Schizochytrium aggregatum.
XX
PN WO200290493-A2.
XX
PD 14-NOV-2002.
XX
PF 02-MAY-2002; 2002WO-US013589.
XX
PR 04-MAY-2001; 2001US-00849199.
PR 11-APR-2002; 2002US-00120637.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Mukerji P, Huang Y, Das T, Thurmond JM, Leonard AB, Pereira SL;
XX
DR WPI; 2003-058927/05.
XX
PT Novel purified Delta4-desaturase enzymes which desaturates
PT polyunsaturated fatty acids at carbon 4, useful for producing

PT polynsaturated fatty acids which are used for treating diabetes, kidney
 XX stones, endometriosis.
 PS Example 7; Page 55; 174pp; English.
 XX
 CC The invention relates to a purified polypeptide, Delta4-desaturase which
 CC desaturates polyunsaturated fatty acids (PUFA) at carbon 4, isolated from
 CC Schizochytrium aggregatum or Thraustochytrium aureum. Also included are
 CC nucleotide sequences encoding the desaturases (including sequences 50%
 CC similar to them), a vector comprising the nucleotide sequence, a host
 CC cell comprising the vector, a transgenic plant cell or tissue comprising
 CC the vector and thereby producing PUFA via expression of the desaturase
 CC and a composition comprising at least omega6-docosapentaenoic acid and
 CC docosahexaenoic acid, produced using the desaturase. The desaturase
 CC protein and nucleotide are useful for producing the final product PUFA
 CC omega6-docosapentaenoic acid or docosahexaenoic acid from the substrate
 CC PUFAs linoleic acid, gamma-linolenic acid, stearidonic acid, arachidonic
 CC acid, dihomo-gamma-linolenic acid, eicosatetraenoic acid, adrenic acid,
 CC or eicosapentaenoic acid. The final product PUFA is omega6-
 CC docosapentaenoic acid and docosahexaenoic acid. The composition is useful
 CC for treating or preventing a condition caused by insufficient intake of
 CC PUFA (e.g. restenosis after angioplasty, inflammation, rheumatoid
 CC arthritis, asthma, psoriasis, osteoporosis, kidney or urinary tract
 CC stones, cancer, cachexia associated with cancer, diabetes, eczema,
 CC gastrointestinal bleeding, endometriosis and premenstrual syndrome,
 CC myalgic encephalomyelitis, chronic fatigue after viral infections,
 CC acquired immunodeficiency syndrome (AIDS), multiple sclerosis and
 CC inflammatory skin disorders). The omega6-Docosapentaenoic acid and
 CC docosahexaenoic acid produced may be added to nutritional compositions
 CC (e.g. infant supplements), pharmaceutical compositions, cosmetics and
 CC animal feeds. The composition is also useful for e.g. reducing blood
 CC pressure, inhibiting platelet aggregation, inducing vasodilation,
 CC reducing cholesterol levels. The present sequence is a PCR primer used to
 CC isolate nucleic acids encoding the delta4-desaturase enzymes of the
 CC invention
 XX
 SQ Sequence 26 BP; 6 A; 4 C; 12 G; 4 T; 0 U; 0 Other;
 Query Match 74.7%; Score 14.2; DB 8; Length 26;
 Best Local Similarity 84.2%; Pred. No. 1.5e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGAGAGGGGGTGGGTGCT 19
 DB 2 GGAGCATGGGTAGGTGCT 20
 RESULT 3
 ABZ70091
 ID ABZ70091 standard; DNA; 30 BP.
 XX
 AC ABZ70091;
 XX
 DT 10-APR-2003 (first entry)
 XX
 DE Human chromosome 22-related PCR primer, 553-F5, SEQ ID 7.
 XX
 KW PCR; primer; human artificial chromosome; antibody lambda light chain;
 KW chromosome 22; human; transgenic; antibody drug; infection; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200292812-A1.
 XX
 PD 21-NOV-2002.
 XX
 PF 10-MAY-2002; 2002WO-JP004587.
 XX
 PR 11-MAY-2001; 2001JP-00142371.
 XX
 PA (KIRI) KIRIN BEER KK.
 PA (MEDA-) MEDAREX INC.
 XX

PI Kuroiwa Y, Tomizuka K, Yoshida H, Ishida I;
 XX WPI; 2003-129293/12.
 XX
 PT Artificial human chromosome containing human antibody lambda light chain
 PT gene transferred to offspring via non-human genital system for
 PT constructing transchromosomic mice, applicable in developing human
 PT antibody drugs.
 XX
 PS Example 5; Page 22; 64pp; Japanese.
 XX
 CC The present invention relates to a human artificial chromosome, which can
 CC be transferred to offspring via a non-human genital system. The human
 CC artificial chromosome carries the antibody lambda light chain gene
 CC (originally from the human chromosome 22) ligated to another chromosome
 CC fragment from another human chromosome. The human artificial chromosome
 CC can be used to generate transgenic mice, which are useful for producing
 CC human antibodies and in developing human antibody drugs for treatment of
 CC e.g. infections. The present sequence is a PCR primer, which was used in
 CC an example from the invention
 XX
 SQ Sequence 30 BP; 12 A; 3 C; 10 G; 5 T; 0 U; 0 Other;
 Query Match 74.7%; Score 14.2; DB 8; Length 30;
 Best Local Similarity 84.2%; Pred. No. 1.5e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGAGAGGGGGTGGGTGCT 19
 DB 2 GAAGAGAGGAGTGGGTGCT 20
 RESULT 4
 AAT86507/c
 ID AAT86507 standard; DNA; 20 BP.
 XX
 AC AAT86507;
 XX
 DT 12-MAR-1998 (first entry)
 XX
 DE S-adenosylmethionine decarboxylase antisense oligonucleotide #8.
 XX
 KW S-adenosylmethionine decarboxylase; SAMDC; antisense oligonucleotide;
 KW antitumour; diagnosis; phosphorothioate; psoriasis; spermine; spermidine;
 KW ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /note= "nucleotides are bonded via phosphorothioate
 FT linkages"
 XX
 PN WO9605298-A1.
 XX
 PD 22-FEB-1996.
 XX
 PF 27-JUL-1995; 95WO-EP002985.
 XX
 PR 09-AUG-1994; 94US-00287753.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Mett H, Haner R, Dean NM;
 XX WPI; 1996-139694/14.
 XX
 PT New oligo:nucleotide derivs. specific for S-adenosyl:methionine
 PT decarboxylase related nucleic acid - useful as anti:sense inhibitors of
 PT this enzyme, esp. for treatment of tumours but also as hybridisation
 PT probes for diagnosis.

XX PS Example 8; Page 45; 81pp; English.

CC This sequence represents a phosphorothioate analogue of an antisense oligonucleotide which targets the 3' untranslated region of S-adenosylmethionine decarboxylase (SAMDC) around nucleotides at positions 1046 to 1065. Antisense oligonucleotide analogues (AAT86500-14) which target the SAMDC gene are used to diagnose conditions associated with expression of SAMDC by specifically hybridising to RNA or DNA derived from the SAMDC gene. These antisense molecules are useful for therapeutic modulation (especially inhibition) of SAMDC synthesis, particularly to treat tumours (e.g. leukaemia, prostatic carcinoma, colon or brain tumours, but especially bladder cancer), but also other hyper-proliferative diseases such as psoriasis. They cause tumour regression and prevent establishment/growth of (micro)metastases. Inhibition of SAMDC reduces the level of polyamines (spermine and spermidine in cells), resulting in cytostasis and possibly apoptosis

CC SQ Sequence 20 BP; 7 A; 8 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 2; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGAAGGGGGTGGTGCT 19
||||| ||||| ||||| |||||
DB 19 AGAAGGTGGTGATGCT 3

RESULT 5

ADK23254

ID ADK23254 standard; DNA; 20 BP.

XX AC ADK23254;

XX DT 18-NOV-2004 (first entry)

XX DE Acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide #3331.

XX KW acyl-coenzyme A synthetase 1; ACS1; diabetes; obesity;
KW metabolic syndrome X; cardiovascular disorder; cancer; infection;
KW inflammation; tumour; antisense; ss.

XX OS Synthetic.

XX PN WO2004016749-A2.

XX PD 26-FEB-2004.

XX PF 14-AUG-2003; 2003WO-US025389.

XX PR 14-AUG-2002; 2002US-0403591P.

XX PA (PHAA) PHARMACIA CORP.

XX PI Ross SA;

XX PS WPI; 2004-203782/19.

XX DR New antisense compounds targeted to nucleic acid molecules encoding acyl-coenzyme A synthetase 1 (ACS1), useful for treating diseases or conditions associated with aberrant expression of ACS1, e.g. diabetes, obesity or cancer.

XX PS Claim 3; SEQ ID NO 3331; 940pp; English.

XX CC The invention relates to an antisense compound targeted to a nucleic acid molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense compound specifically hybridises with and inhibits the expression of ACS1. The antisense oligonucleotides or compounds are useful for inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for treating diseases or conditions associated with aberrant expression of ACS1, e.g. diabetes, obesity, metabolic syndrome X, cardiovascular

CC disorder or cancer. The antisense compounds are also useful as research reagents and kits, or in diagnostic, therapeutic and prophylactic applications, e.g. to prevent or delay infection, inflammation or tumour formation. The present sequence represents an acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide.

CC SQ Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 13; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGAAGGGGGTGGTGCT 19
||||| ||||| ||||| |||||
DB 3 AGAAGGTGGTGATGCT 19

RESULT 6

ADK23371

ID ADK23371 standard; DNA; 20 BP.

XX AC ADK23371;

XX DT 18-NOV-2004 (first entry)

XX DE Acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide #3448.

XX KW acyl-coenzyme A synthetase 1; ACS1; diabetes; obesity;
KW metabolic syndrome X; cardiovascular disorder; cancer; infection;
KW inflammation; tumour; antisense; ss.

XX OS Synthetic.

XX PN WO2004016749-A2.

XX PD 26-FEB-2004.

XX PF 14-AUG-2003; 2003WO-US025389.

XX PR 14-AUG-2002; 2002US-0403591P.

XX PA (PHAA) PHARMACIA CORP.

XX PI Ross SA;

XX PS WPI; 2004-203782/19.

XX DR New antisense compounds targeted to nucleic acid molecules encoding acyl-coenzyme A synthetase 1 (ACS1), useful for treating diseases or conditions associated with aberrant expression of ACS1, e.g. diabetes, obesity or cancer.

XX PS Claim 3; SEQ ID NO 3448; 940pp; English.

XX CC The invention relates to an antisense compound targeted to a nucleic acid molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense compound specifically hybridises with and inhibits the expression of ACS1. The antisense oligonucleotides or compounds are useful for inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for treating diseases or conditions associated with aberrant expression of ACS1, e.g. diabetes, obesity, metabolic syndrome X, cardiovascular

CC disorder or cancer. The antisense compounds are also useful as research reagents and kits, or in diagnostic, therapeutic and prophylactic applications, e.g. to prevent or delay infection, inflammation or tumour formation. The present sequence represents an acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide.

CC SQ Sequence 20 BP; 5 A; 2 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 13; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 3 AGAAGGGGTGGTGCT 19
Db 1 AGAAGGTGGTGAGTGCT 17

RESULT 7
ID ADK23372
AC ADK23372 standard; DNA; 20 BP.
XX
XX ADK23372;
XX
XX 18-NOV-2004 (first entry)
XX
DE Acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide #3449.
XX
XX acyl-coenzyme A synthetase 1; ACS1; diabetes; obesity;
KW metabolic syndrome X; cardiovascular disorder; cancer; infection;
KW inflammation; tumour; antisense; ss.
XX
OS Synthetic.
XX
PN WO2004016749-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025389.
XX
XX 14-AUG-2002; 2002US-0403591P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Ross SA;
XX
XX WPI; 2004-203782/19.
XX
XX New antisense compounds targeted to nucleic acid molecules encoding acyl-
PT coenzyme A synthetase 1 (ACS1), useful for treating diseases or
PT conditions associated with aberrant expression of ACS1, e.g. diabetes,
PT obesity or cancer.
XX
XX Claim 3; SEQ ID NO 3449; 940pp; English.
XX
XX The invention relates to an antisense compound targeted to a nucleic acid
CC molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense
CC compound specifically hybridises with and inhibits the expression of
CC ACS1. The antisense oligonucleotides or compounds are useful for
CC inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for
CC treating diseases or conditions associated with aberrant expression of
CC ACS1, e.g. diabetes, obesity, metabolic syndrome X, cardiovascular
CC disorder or cancer. The antisense compounds are also useful as research
CC reagents and kits, or in diagnostic, therapeutic and prophylactic
CC applications, e.g. to prevent or delay infection, inflammation or tumour
CC formation. The present sequence represents an acyl-coenzyme A synthetase
CC 1, ACS1, antisense oligonucleotide.
XX
SQ Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 72.6%; Score 13.8; DB 13; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGTGCT 19
Db 2 AGAAGGTGGTGAGTGCT 18

RESULT 8
ID ADK23389
AC ADK23389 standard; DNA; 20 BP.
XX
XX ADK23389;
XX
XX 18-NOV-2004 (first entry)
XX

QY 3 AGAAGGGGTGGTGCT 19
Db 4 AGAAGGTGGTGAGTGCT 20

RESULT 9
AEF42976/c
ID AEF42976 standard; DNA; 20 BP.
XX
XX AEF42976;
AC
XX
XX 23-MAR-2006 (first entry)
XX
XX Mesoblast-specific transcript (Mest) cDNA PCR primer #2.
XX
XX Diagnosis; therapeutic; mesoblast-specific transcript; Mest; adipocyte;
KW obesity; non-insulin dependent diabetes; arteriosclerosis; hypertension;
KW hyperlipidemia; PCR; primer; ss; antidiabetic; antiarteriosclerotic;
KW hypotensive; antilipemic; anorectic.
XX
XX Synthetic.
XX
XX WO2006006389-A1.
PN
XX
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PD 19-JAN-2006.
XX
XX
PF 28-JUN-2005; 2005WO-JP011810.
XX
XX 08-JUL-2004; 2004JP-00201895.
XX
XX (NIHE-) JAPAN HEALTH SCI FOUND.
XX
XX Takahashi M, Kamei Y, Ezaki O;
XX
XX WPI; 2006-110104/11.
XX
XX Diagnosing obesity-related diseases by measuring expression of mesoblast-
XX specific transcript (Mest) in adipocytes, useful in clinical examination
XX and in screening drugs in the treatment of, e.g. diabetes.
XX
XX Disclosure; SEQ ID NO 2; 34pp; Japanese.
XX
XX The invention relates to a method of diagnosing obesity-related diseases
XX comprising measuring the expression doses of mesoblast-specific
XX transcript (Mest) in adipocytes. The invention also relates to a method
XX of examining whether or not a test substance is a Mest expression
XX controller comprising the administration of the test substance to an
XX animal for laboratory use, measuring the amount of Mest mRNA in
XX adipocytes of the animal or the amount of Mest protein in its blood and
XX determining whether or not the test substance can cause a change in the
XX Mest mRNA expression dose, and a method of screening a Mest expression
XX controller. To assay the Mest expression dose, the amount of Mest mRNA in
XX adipocytes or the amount of Mest protein in blood is measured. The method
XX is useful in clinical examination and in screening of expression
XX controllers as drugs in the treatment or management of, e.g. obesity,
XX type II diabetes, arteriosclerosis, hypertension and hyperlipemia. This
XX sequence represents a PCR primer used to amplify Mest cDNA of the
XX invention.
XX
XX Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 15; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGCT 19
Db 19 AGAAGTGGGTGAGTCT 3

RESULT 10
ADN00574/c
ID ADN00574 standard; DNA; 21 BP.
XX
XX AC ADN00574;
XX
XX 17-JUN-2004 (first entry)
XX
XX Murine adipocyte P2 (ap2) PCR primer #2.
XX
XX Osteoblastic differentiation induction; osteoblastic differentiation;
XX mesenchymal stem cell; oxysterol; adipocyte differentiation inhibition;
XX adipocyte differentiation; adipogenesis; adipogenic gene;
XX lipoprotein lipase; LPL; adipocyte P2; ap2; murine; PCR; primer; ss.
XX
XX Mus sp.
XX
XX WO2004019884-A2.
XX
XX 11-MAR-2004.
XX
XX 28-AUG-2003; 2003WO-US027105.
XX
XX 29-AUG-2002; 2002US-0406715P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX

PI Parhami F;
XX
XX WPI; 2004-257333/24.
XX
XX Use of oxysterol to induce osteoblastic differentiation and bone
XX formation to increase bone mass and inhibit adipocyte differentiation in
XX mammalian mesenchymal stem cells.
XX
XX Disclosure; Page 15; 47pp; English.
XX
XX The present invention relates to a method for induction of osteoblastic
XX differentiation in mammalian mesenchymal stem cells. The method comprises
XX administration of at least one oxysterol (A). (A) is used to induce
XX osteoblastic differentiation and inhibit adipocyte differentiation in
XX mammalian mesenchymal stem cells and treat mammalian mesenchymal cells.
XX (A) is administered at a selected interval together with at least one
XX secondary agent (such as parathyroid hormone, sodium fluoride, insulin-
XX like growth factor I, insulin-like growth factor II or transforming
XX growth factor beta) to increase the differentiation of marrow stromal
XX cells into osteoblasts and to increase the number of osteoblasts present
XX in bone tissue, induce bone formation to increase bone mass and treat
XX osteoporosis to ameliorate the symptoms of osteoporosis. In an example
XX from the invention, adipogenesis was assessed by an inhibition of
XX expression of adipogenic genes lipoprotein lipase (LPL) and adipocyte P2
XX (ap2) by (A) using PCR primers ADN00573-ADN00576.
XX
XX Sequence 21 BP; 4 A; 10 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 12; Length 21;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGCT 19
Db 18 AGAAGTGGGTGAGTCT 2

RESULT 11
ADY38715/c
ID ADY38715 standard; DNA; 21 BP.
XX
XX AC ADY38715;
XX
XX 19-MAY-2005 (first entry)
XX
XX Mouse adipocyte protein 2 (ap2) PCR primer #2.
XX
XX differentiation; stem cell; osteopathic; bone repair; bone degeneration;
XX osteoporosis; ap2; adipocyte protein 2; PCR; primer; ss.
XX
XX Mus musculus.
XX
XX WO2005020928-A2.
XX
XX 10-MAR-2005.
XX
XX 30-AUG-2004; 2004WO-US028162.
XX
XX 29-AUG-2003; 2003US-0499040P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Parhami F;
XX
XX WPI; 2005-214410/22.
XX
XX Induction of osteoblastic differentiation of mammalian mesenchymal stem
XX cells includes treating mammalian mesenchymal cells with at least one
XX oxysterol and at least one bone morphogenic protein.
XX
XX Example; Page 16; 52pp; English.
XX
XX This invention relates to a novel method of induction of osteoblastic

```


CC differentiation of mammalian mesenchymal stem cells. The method includes
 CC treating mammalian mesenchymal cells with at least one oxysterol and at
 CC least one bone morphogenic protein (BMP). The invention may be useful for
 CC the development of compounds with an osteopathic activity acting as
 CC adipocyte differentiation of MSC inhibitors, osteoblastic differentiation
 CC of MSC inducers or Liver X receptors (LXR) activators. The invention may
 CC be useful to induce osteoblastic differentiation of mammalian mesenchymal
 CC stem cells (MSC), to stimulate mammalian cells to express a level of a
 CC biological marker of osteoblastic differentiation, to inhibit adipocyte
 CC differentiation of MSC, to increase the differentiation of marrow stromal
 CC cells into osteoblasts and to induce bone formation (endochondral or
 CC intramembraneous bone formation) and to treat/ameliorate a patient
 CC exhibiting clinical symptoms of osteoporosis. The method is very
 CC effective in treating bone disorders without side effects. The present
 CC sequence is that of a PCR primer which was used for amplification of a
 CC region of the mouse adipocyte protein 2 (ap2)-encoding gene in the
 CC exemplification of the invention.

XX Sequence 21 BP; 4 A; 10 C; 1 G; 6 T; 0 U; 0 Other;
 SQ Query Match 72.6%; Score 13.8; DB 14; Length 21;
 Best Local Similarity 88.2%; Pred. No. 2.2e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGAAGGGGTGGTGCT 19
 Db 18 AGAAGTGGGTGAGTGCT 2
 ||||| ||||| |||||

RESULT 12
 ADW43979/c
 ID ADW43979 standard; DNA; 23 BP.

XX AC ADW43979;

DT 24-MAR-2005 (first entry)

DE Human MODY 1 gene exon 4 amplifying forward primer, Mle4f3n.

XX Gene amplification; SNP detection;
 KW maturity-onset diabetes mellitus in the young; MODY gene 1; PCR; primer;
 KW ss.

XX OS Homo sapiens.

XX PN US2005003418-A1.

XX PD 06-JAN-2005.

XX PF 19-JUN-2004; 2004US-00871302.

XX PR 17-JUN-2003; 2003KR-00039125.

XX PA (KIMM/) KIM M.

XX PA (HANH/) HAN H.

XX PA (KIMS/) KIM S.

XX PA (JEON/) JEONG S.

XX PA (KIMK/) KIM K.

XX PA (LEEJ/) LEE J.

XX PA (CHOI/) CHOI Y.

XX Kim M, Han H, Kim S, Jeong S, Kim K, Lee J, Choi Y;

XX WPI; 2005-065236/07.

XX New primer pool including at least two sets of primers, useful for
 XX amplifying human MODY gene 1, 4, 5, 6, or 7.
 XX Claim 1; SEQ ID NO 5; 23pp; English.

XX The invention relates to a primer pool which includes at least two sets
 CC of primers for amplifying at least two target sequences of human MODY
 CC (maturity-onset diabetes mellitus in the young) gene 1, 4, 5, 6 or 7. The

CC primer pool, method and kit are useful for amplifying target sequences,
 CC specifically for amplifying human MODY gene 1, 4, 5, 6 or 7. The present
 CC sequence is a primer used to amplify human MODY gene 1 exon 4 sequence.
 XX Sequence 23 BP; 6 A; 14 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 14; Length 23;
 Best Local Similarity 88.2%; Pred. No. 2.2e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CGAGAAGGGGTGGGTG 17
 Db 22 CGAGTAGGGGGTGGGG 6
 ||||| ||||| |||||

RESULT 13

ADZ87881/c

ID ADZ87881 standard; RNA; 19 BP.

XX AC ADZ87881;

DT 28-JUL-2005 (first entry)

DE Early growth response gene (Egr-1) siRNA molecule #94.

XX RNA interference; gene silencing; short interfering RNA; siRNA;
 KW early growth response; Egr-1; angiogenesis disorder; cancer;
 KW breast tumor; lung tumor; bladder tumor; skin tumor; brain tumor;
 KW epithelial carcinoma; melanoma; diabetic retinopathy;
 KW age related macular degeneration; neovascular glaucoma;
 KW myopic degeneration; arthritis; psoriasis; endometriosis;
 KW gynecology and obstetrics; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; port-wine stain; Sturge-Weber syndrome;
 KW Klippel-Trenaunay-Weber syndrome; hereditary hemorrhagic telangiectasia;
 KW renal disease; polycystic kidney disease; restenosis; arteriosclerosis;
 KW cytostatic; ophthalmological; antidiabetic; antiarrhythmic;
 KW dermatological; virucide; cerebroprotective; vasotropic; hemostatic;
 KW osteoarthritic; antiangiogenic; antipsoriatic; gynecological;
 KW antiarteriosclerotic; nephrotropic; ds.

XX OS Homo sapiens.

XX PN WO2005045032-A2.

XX PD 19-MAY-2005.

XX PF 19-AUG-2004; 2004WO-US026941.

XX PR 20-OCT-2003; 2003US-0512701P.

XX PR 23-OCT-2003; 2003US-00693059.

XX PR 24-NOV-2003; 2003US-00720448.

XX PR 03-DEC-2003; 2003US-00727780.

XX PR 14-JAN-2004; 2004US-00757803.

XX PR 10-FEB-2004; 2004US-0543480P.

XX PR 13-FEB-2004; 2004US-00780447.

XX PR 16-APR-2004; 2004US-00826966.

XX PR 30-APR-2004; 2004WO-US013456.

XX PR 24-MAY-2004; 2004WO-US016390.

XX PA (SIMA-) SIMA THERAPEUTICS INC.

XX Usman N, Mcswiggen J;

XX WPI; 2005-356234/36.

XX New short interfering nucleic acid molecule that directs cleavage of an
 XX early growth response RNA, useful for treating cancer, ocular disease,
 XX proliferative condition, renal disease or arteriosclerosis.
 XX Claim 33; SEQ ID NO 94; 200pp; English.

XX The invention relates to a chemically synthesized double stranded short
 CC interfering nucleic acid (siRNA) molecule that directs cleavage of an

CC early growth response (Egr-1) RNA via RNA interference (RNAi). The
CC invention also relates to a composition comprising the siRNA molecule with
CC a pharmaceutical carrier or diluent. The siRNA molecule is useful for
CC treating tumor angiogenesis and cancer, e.g., breast, lung, bladder,
CC skin, and brain cancer, epithelial carcinoma, and melanoma. The molecule
CC is also useful for treating diabetic retinopathy, age related macular
CC degeneration, neovascular glaucoma, myopic degeneration, arthritis,
CC psoriasis, endometriosis, female reproductive disorders, verruca
CC vulgaris, angiofibroma, tuberous sclerosis, port-wine stains, Sturge-
CC Weber syndrome, Klippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu
CC syndrome, renal disease, polycystic kidney disease, restenosis and
CC arteriosclerosis. This sequence represents an Egr-1 siRNA molecule of the
CC invention.

XX Sequence 19 BP; 1 A; 10 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 70.5%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGG 15

DB 19 GGAGAGGGGGTGGG 5

RESULT 14

ADZ8055

ID ADZ8055 standard; RNA; 19 BP.

AC ADZ88055;

XX 28-JUL-2005 (first entry)

DE Early growth response gene (Egr-1) siRNA molecule #269.

XX RNA interference; gene silencing; short interfering RNA; siRNA;
KW early growth response; Egr-1; angiogenesis disorder; cancer;
KW breast tumor; lung tumor; bladder tumor; skin tumor; brain tumor;
KW epithelial carcinoma; melanoma; diabetic retinopathy;
KW age related macular degeneration; neovascular glaucoma;
KW myopic degeneration; arthritis; psoriasis; endometriosis;
KW gynecology and obstetrics; verruca vulgaris; angiofibroma;
KW tuberous sclerosis; port-wine stain; Sturge-Weber syndrome;
KW Klippel-Trenaunay-Weber syndrome; hereditary hemorrhagic telangiectasia;
KW renal disease; polycystic kidney disease; restenosis; arteriosclerosis;
KW cytostatic; ophthalmological; antidiabetic; antiarthritic;
KW dermatological; virucide; cerebroprotective; vasotrophic; hemostatic;
KW osteopathic; antiangiogenic; antipsoriatic; gynecological;
KW antiarteriosclerotic; nephrotropic; ds.

XX Homo sapiens.

XX WO2005045032-A2.

XX 19-MAY-2005.

XX 19-AUG-2004; 2004WO-US026941.

XX 20-OCT-2003; 2003US-0512701P.

XX 23-OCT-2003; 2003US-00693059.

XX 24-NOV-2003; 2003US-00720448.

XX 03-DEC-2003; 2003US-00727780.

XX 14-JAN-2004; 2004US-00757803.

XX 10-FEB-2004; 2004US-0543480P.

XX 13-FEB-2004; 2004US-00780447.

XX 16-APR-2004; 2004US-00826966.

XX 30-APR-2004; 2004WO-US013456.

XX 24-MAY-2004; 2004WO-US016390.

XX (SINA-) SINA THERAPEUTICS INC.

XX Usman N, Mcswiggen J;

XX

DR WPI; 2005-356234/36.

XX New short interfering nucleic acid molecule that directs cleavage of an
XX early growth response RNA, useful for treating cancer, ocular disease,
XX proliferative condition, renal disease or arteriosclerosis.

PS Claim 33; SEQ ID NO 269; 200pp; English.

XX The invention relates to a chemically synthesized double stranded short
XX interfering nucleic acid (siRNA) molecule that directs cleavage of an
XX early growth response (Egr-1) RNA via RNA interference (RNAi). The
XX invention also relates to a composition comprising the siRNA molecule with
XX a pharmaceutical carrier or diluent. The siRNA molecule is useful for
XX treating tumor angiogenesis and cancer, e.g., breast, lung, bladder,
XX skin, and brain cancer, epithelial carcinoma, and melanoma. The molecule
XX is also useful for treating diabetic retinopathy, age related macular
XX degeneration, neovascular glaucoma, myopic degeneration, arthritis,
XX psoriasis, endometriosis, female reproductive disorders, verruca
XX vulgaris, angiofibroma, tuberous sclerosis, port-wine stains, Sturge-
XX Weber syndrome, Klippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu
XX syndrome, renal disease, polycystic kidney disease, restenosis and
XX arteriosclerosis. This sequence represents an Egr-1 siRNA molecule of the
XX invention.

SQ Sequence 19 BP; 6 A; 2 C; 10 G; 0 T; 1 U; 0 Other;

Query Match 70.5%; Score 13.4; DB 14; Length 19;

Best Local Similarity 86.7%; Pred. No. 3.3e+04;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGG 15

DB 1 GGAGAGGGGGTGGG 15

RESULT 15

AEB43635

ID AEB43635 standard; RNA; 19 BP.

XX AC AEB43635;

XX 22-SEP-2005 (first entry)

DE Novel human Egr-1 gene-targeting siRNA sequence SeqID268.

XX antiarthritic; vasotropic; antiinflammatory; ophthalmological;
XX antidiabetic; antipsoriatic; cerebroprotective; antiarteriosclerotic;
KW cancer; ocular disease; tumor; angiogenesis; angiogenesis;
KW hyperproliferation; diabetic retinopathy; macular degeneration; aging;
KW arthritis; psoriasis; sturge-weber syndrome; restenosis;
KW arteriosclerosis; RNA interference; gene silencing;
KW short interfering RNA; siRNA; cytostatic; drug screening; diagnostic;
KW genetic engineering; gene mapping; Egr-1; ss.

XX Homo sapiens.

XX US2005153915-A1.

XX 14-JUL-2005.

XX 19-AUG-2004; 2004US-00922544.

XX 18-MAY-2001; 2001US-0292217P.

XX 20-JUL-2001; 2001US-0306883P.

XX 13-AUG-2001; 2001US-0311865P.

XX 20-FEB-2002; 2002US-0358580P.

XX 06-MAR-2002; 2002US-0362016P.

XX 11-MAR-2002; 2002US-0363124P.

XX 20-MAY-2002; 2002WO-US015876.

XX 06-JUN-2002; 2002US-0386782P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

an siRNA of the invention. The siRNAs are used to modulate expression of the Egr-1 gene in cells, tissue explants or organisms (for example by ex vivo gene therapy), or in grafts and transplants for the treatment of a variety of conditions. The siRNAs may be useful for the development of compounds with a cytostatic, antiarthritic, vasotropic, antiinflammatory, ophthalmological, antidiabetic, antipsoriatic, cerebroprotective or antiarteriosclerotic activity acting by RNA interference. They may be used in the treatment of cancer (for example colorectal cancer, adenocarcinoma, lymphoma and glioma), ocular disease (for example toxic conjunctivitis, bacterial keratitis, uveitic glaucoma and squamous cell carcinoma), tumor angiogenesis, and proliferative conditions such as diabetic retinopathy, macular degeneration, age related macular degeneration, arthritis, psoriasis, Sturge Weber syndrome, restenosis and/or arteriosclerosis. The siRNAs may also be used in drug screening, diagnosis, therapeutic target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single nucleotide polymorphisms). The present sequence is that of a human Egr-1 gene-targeting siRNA of the invention.

Sequence 19 BP; 1 A; 10 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 70.5%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGG 15

Db 19 GGAGAGGGGGTGGG 5

RESULT 17
AAD45780/c
ID AAD45780 standard; DNA; 22 BP.

XX AAD45780;

XX 27-DEC-2002 (first entry)

XX Human promoter -147 CYP4503A5 specific probe #1.

XX Human; cytochrome P450; CYP3A4; CYP3A5; glutathione S-transferase;
KW polymorphism; GSTM1; breast cancer; therapy; chemotherapeutic agent;
KW drug-drug interaction; drug adverse effect; anti-cancer agent; enzyme;
KW probe; promoter; ss.

XX Homo sapiens.

XX WO200268448-A1.

XX 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US006135.

XX 26-FEB-2001; 2001US-0271630P.

XX (DNAS-) DNA SCI INC.

XX (UYDU-) UNIV DUKE.

XX Guida M, Hall J, Petros WP, Vredenburg JJ, Colvin OM, Marks JR;

XX WPI; 2002-691652/74.

XX New nucleic acid molecule useful for identifying polymorphisms associated
PT with CYP3A4, CYP3A5 or GSTM1 substrates which influence breast cancer
PT treatments, comprises at least one base variation from human CYP3A4 or
PT CYP3A5 sequence.

XX Example 3; Page 27; 41pp; English.

XX The invention relates to a nucleic acid molecule comprising at least one
CC base variation from human cytochrome P450 (CYP) 3A4 or CYP3A5 sequence.
CC Nucleic acid molecules of the invention are useful for identifying
CC polymorphisms associated with CYP3A4, CYP3A5 or glutathione S-transferase

CC (GST) M1 substrates which influence breast cancer treatments. They are
CC also useful in diagnostic purposes to identify individuals having a
CC polymorphic genotype which influence the outcome of breast cancer
CC treatments and the selection of chemotherapeutic agents used to treat
CC breast cancer. The polymorphisms detected are used to screen altered
CC metabolism of CYP3A4, CYP3A5 or GSTM1 substrates, potential drug-drug
CC interactions, drug adverse effects, likelihood of successful clinical
CC outcome following treatment with anti-cancer agents such as cisplatin,
CC cyclophosphamide and/or BCNU. The present sequence is human promoter -147
CC CYP4503A5 specific probe

XX Sequence 22 BP; 2 A; 13 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 70.5%; Score 13.4; DB 6; Length 22;

Best Local Similarity 93.3%; Pred. No. 3.3e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGG 15

Db 22 GGAGAGGGGGTGGG 8

RESULT 18
AAZ75471/c
ID AAZ75471 standard; DNA; 18 BP.

XX AAZ75471;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID NO:9827.

XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.

XX Claim 8; Page 2325; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

```
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 3 A; 8 C; 1 G; 6 T; 0 U; 0 Other;

Query Match          69.5%; Score 13.2; DB 3; Length 18;
Best Local Similarity 83.3%; Pred. No. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTGCT 19
   ||||| ||| |||||
Db 18 GAGAGGGAGGTAAGTCT 1

RESULT 19
ADI57107/c
ID ADI57107 standard; DNA; 20 BP.
XX
AC ADI57107;
XX
XX
XX 22-APR-2004 (first entry)
XX
DE Oryza minuta Pi9 locus nucleotide binding site (NBS) gene PCR primer #24.
XX
KW nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant; PCR; primer; ss.
XX
OS Oryza minuta.
XX
PN US2004006788-A1.
XX
XX 08-JAN-2004.
XX
XX 27-JAN-2003; 2003US-00352179.
XX
XX 25-JAN-2002; 2002US-0352108P.
XX
PR 01-FEB-2002; 2002US-0353304P.
XX
XX (WANG/) WANG G.
XX (LIU/) LIU G.
XX
XX Wang G, Liu G;
XX
XX WPI; 2004-121064/12.
XX
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
XX and NBS3, useful for producing plants resistant to Magnaporthe grisea
XX infection.
XX
XX Disclosure; SEQ ID NO 24; 136pp; English.
XX
XX The invention comprises the amino acid and coding sequences of nucleotide
XX binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
XX blight and rice blast resistance genes). The DNA sequences may be used as
XX markers for resistance to infection with Magnaporthe grisea in plant
XX breeding programs. The present DNA sequence represents a PCR primer for
XX the Oryza minuta Pi9 locus.
XX
XX Sequence 20 BP; 6 A; 10 C; 2 G; 2 T; 0 U; 0 Other;

Query Match          69.5%; Score 13.2; DB 12; Length 20;
Best Local Similarity 83.3%; Pred. No. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTGCT 19
   ||||| ||| |||||
Db 20 GAGATGGGTGGGTGCT 3

RESULT 20
ABA00323
ID ABA00323 standard; cDNA; 21 BP.
XX
```

```
AC ABA00323;
XX
XX 09-DEC-2002 (first entry)
XX
DE cDNA encoding TCR beta-chain N-D-N junction region from donor UA.
XX
KW Transcription factor; STAT-1; monocyte; unstable angina; UA;
KW stable angina; SA; SIE oligonucleotide; sis-inducible element;
KW interferon; IFN-gamma; unstable plaque; cardiovascular condition; angina;
KW PCR; primer; amplify; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..21
XX FT /*tag= a
XX FT /partial
XX
XX WO2000267766-A2.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002WO-US005760.
XX
XX 23-FEB-2001; 2001US-00792686.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
XX Goronzy JJ, Weyand CM, Kopecky SL;
XX
XX WPI; 2002-698620/75.
XX
XX P-FSDB; AAG79536.
XX
XX Determining whether or not a mammal has an unstable plaque, useful for
XX evaluating the severity of cardiovascular conditions, e.g. angina,
XX comprises determining the level of CD64 or IP-10 polypeptide encoded by
XX DNA responsive to STAT-1.
XX
XX Example 8; Page 29; 49pp; English.
XX
XX The sequences given in ABA00318-27 are sequences which encode the N-D-N
XX junction region at the interface of TCR-BV and -BJ gene segments in
XX unstable angina (UA) patients. All these sequences have shared amino acid
XX sequence homology and display heterogeneity at the nucleotide level.
XX Sequences like these were identified using the method of the invention
XX for determining if a mammal has an unstable plaque. The method comprises
XX determining whether or not a sample from the mammal contains an elevated
XX level of a polypeptide which is encoded by a DNA responsive to an
XX interferon-gamma-activated transcription factor. The level indicates that
XX the mammal contains the unstable plaque. The method is useful in
XX evaluating the severity of cardiovascular conditions, such as angina,
XX specifically by determining whether a person has an unstable plaque. The
XX method may also be used to identify compounds that are useful in treating
XX breeding programs, or reducing the risk of developing life-threatening cardiovascular
XX conditions
XX
XX Sequence 21 BP; 3 A; 4 C; 11 G; 3 T; 0 U; 0 Other;

Query Match          69.5%; Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3%; Pred. No. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTGCT 19
   ||||| ||| |||||
Db 2 GCGAAGGGGGGGGTCT 19

RESULT 21
AAV72586
ID AAV72586 standard; DNA; 25 BP.
XX
XX AAV72586;
XX
```

DT 15-MAR-1999 (first entry)
 XX NOXR1 cDNA specific primer IIA.
 DE
 XX NOXR1; antimicrobial resistance; tuberculosis; macrophage; vaccine;
 KW septic hypotension; stroke; therapy; PCR; primer; ss.
 KW
 XX Synthetic.
 OS Mycobacterium tuberculosis.
 XX
 PN WO9850402-A1.
 XX
 XX 12-NOV-1998.
 PD
 XX 28-APR-1998; 98WO-US008497.
 PF
 XX 06-MAY-1997; 97US-0045688P.
 XX
 XX (CORR) CORNELL RES FOUND INC.
 PA
 XX Riley LW, Nathan CF, Ehrst S;
 PI
 XX WPI; 1999-034703/03.
 DR
 XX DNA conferring resistance on Mycobacterium tuberculosis - to
 PT antimicrobial reactive oxygen and nitrogen intermediates, used for
 PT vaccinating mammals against Mycobacterium.
 XX
 XX Example 8; Page 29; 80pp; English.
 PS
 XX This is the nucleotide sequence of primer IIA that is specific for NOXR1
 CC cDNA (see AAV72577) of Mycobacterium tuberculosis. Primer sets Ia and Ib
 CC (see AAV72584-85), and IIA and IIB (see AAV72587), were used in RT-PCR to
 CC demonstrate expression of recombinant NOXR1 in Mycobacterium smegmatis
 CC and of native NOXR1 in M. tuberculosis. NOXR1 confers resistance to
 CC antibacterial reactive nitrogen and oxygen intermediates. NOXR1 nucleic
 CC acids, polypeptides (see AA83357) and antibodies can be used in the
 CC production of vaccines, in diagnostic methods, and in methods for
 CC treating septic hypotension and stroke, and for quenching overproduction
 CC of nitric oxide in response to infection
 XX
 XX Sequence 25 BP; 1 A; 3 C; 16 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 69.5%; Score 13.2; DB 2; Length 25;
 Best Local Similarity 83.3%; Pred. NO. 4e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGAGAGGGGGTGGGTGC 18
 DB 1 GGGGATGGCGTGGGTGC 18
 RESULT 22
 ADO12772/c
 ID ADO12772 standard; DNA; 30 BP.
 XX
 AC ADO12772;
 XX
 DT 15-JUL-2004 (first entry)
 DE
 XX Single multiplex PCR primer #2144.
 DE
 XX ss; primer; simultaneous amplification;
 KW single multiplex polymerase chain reaction; multifactorial disease;
 KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
 KW gene expression profiling.
 KW
 XX Synthetic.
 OS
 XX WO2004033649-A2.
 PN
 XX 22-APR-2004.
 PD
 XX

PF 07-OCT-2003; 2003WO-US031874.
 XX
 PR 07-OCT-2002; 2002US-0417009P.
 XX
 PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 XX
 PI Li H, Li J;
 XX
 DR WPI; 2004-340914/31.
 XX
 XX Designing primers for simultaneous amplification of target DNA fragments
 PT in a single multiplex polymerase chain reaction, for high throughput
 PT multiplex DNA sequence amplification, comprises aligning two primers.
 XX
 XX Disclosure; Page 43; 120pp; English.
 PS
 XX The invention relates to a method of designing primers for simultaneous
 CC amplification of target DNA fragments in a single multiplex polymerase
 CC chain reaction by aligning a first primer and a second primer. The method
 CC comprises: (a) aligning a first primer and a second primer; and (b)
 CC selecting the first primer where the first primer at its 3' end does not
 CC contain four or more bases that are perfectly matching to the 3' end
 CC sequence of the first primer or a second primer, the first primer at its
 CC 3' end does not contain seven or more bases that are perfectly matching
 CC except one mismatch to the 3' end sequence of the first primer or the
 CC second primer, the first primer at its 3' end does not contain six or
 CC more bases that are perfectly matching to a sequence anywhere of the
 CC first primer or the second primer, and the first primer at its 3' end
 CC does not contain eleven or more bases that are perfectly matching except
 CC one mismatch to a sequence anywhere of the first primer or the second
 CC primer. The method is useful for designing primers for simultaneous
 CC amplification of target DNA fragments in a single multiplex polymerase
 CC chain reaction. It is also useful in the identification of multiple genes
 CC related to multifactorial diseases, the genome-scale detection of genetic
 CC alterations, the studies in pharmacogenetic reactions, the genotyping
 CC genetic polymorphisms in a large population, the gene expression
 CC profiling in various samples and high throughput genotyping technologies.
 CC This sequence corresponds to an example of a primer of the invention.
 XX
 XX Sequence 30 BP; 5 A; 10 C; 4 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 69.5%; Score 13.2; DB 12; Length 30;
 Best Local Similarity 83.3%; Pred. NO. 4e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GAGAGGGGGTGGGTGCT 19
 DB 19 GAGAGGGGATAGGTGCT 2
 RESULT 23
 ADO12782
 ID ADO12782 standard; DNA; 30 BP.
 XX
 AC ADO12782;
 XX
 DT 15-JUL-2004 (first entry)
 DE
 XX Single multiplex PCR primer #2154.
 DE
 XX ss; primer; simultaneous amplification;
 KW single multiplex polymerase chain reaction; multifactorial disease;
 KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
 KW gene expression profiling.
 KW
 XX Synthetic.
 OS
 XX WO2004033649-A2.
 PN
 XX 22-APR-2004.
 PD
 XX 07-OCT-2003; 2003WO-US031874.
 PF
 XX

PR 07-OCT-2002; 2002US-0417009P.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Li H, Li J;
XX WPI; 2004-340914/31.
XX Designing primers for simultaneous amplification of target DNA fragments
PT in a single multiplex polymerase chain reaction, for high throughput
PT multiplex DNA sequence amplification, comprises aligning two primers.
XX
PS Disclosure; Page 43; 120pp; English.
XX
XX The invention relates to a method of designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction by aligning a first primer and a second primer. The method
CC comprises: (a) aligning a first primer and a second primer; and (b)
CC selecting the first primer where the first primer at its 3' end does not
CC contain four or more bases that are perfectly matching to the 3' end
CC sequence of the first primer or a second primer, the first primer at its
CC 3' end does not contain seven or more bases that are perfectly matching
CC except one mismatch to the 3' end sequence of the first primer or the
CC second primer, the first primer at its 3' end does not contain six or
CC more bases that are perfectly matching to a sequence anywhere of the
CC first primer or the second primer, and the first primer at its 3' end
CC does not contain eleven or more bases that are perfectly matching except
CC one mismatch to a sequence anywhere of the first primer or the second
CC primer. The method is useful for designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction. It is also useful in the identification of multiple genes
CC related to multifactorial diseases, the genome-scale detection of genetic
CC alterations, the studies in pharmacogenetic reactions, the genotyping
CC genetic polymorphisms in a large population, the gene expression
CC profiling in various samples and high throughput genotyping technologies.
XX This sequence corresponds to an example of a primer of the invention.
XX
XX Sequence 30 BP; 11 A; 4 C; 10 G; 5 T; 0 U; 0 Other;
SQ
Query Match 69.5%; Score 13.2; DB 12; Length 30;
Best Local Similarity 83.3%; Pred. No. 4e+04; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 3; Indels 0; Gaps 0;
OY 2 GAGAGGGGGTGGGTCT 19
Db 12 GAGAGGGATAGGGTCT 29
|||||
|||||
RESULT 24
ABC22092
ID ABC22092 standard; DNA; 13 BP.
XX AC ABC22092;
XX
XX ABC22092;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 22109 for detecting SNP TSC0004396.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 22109; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 9 G; 1 T; 0 U; 0 Other;
SQ
Query Match 68.4%; Score 13; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+04; Mismatches 0; Gaps 0;
Matches 13; Conservative 0; Indels 0; Indels 0; Gaps 0;
OY 3 AGAAGGGGGTGGG 15
Db 1 AGAAGGGGGTGGG 13
|||||
|||||
RESULT 25
ABC22093/c
ID ABC22093 standard; DNA; 13 BP.
XX AC ABC22093;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 22110 for detecting SNP TSC0004396.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 22110; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 9 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 68.4%; Score 13; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGG 15
|||||||
Db 13 AGAAGGGGGTGGG 1

RESULT 26

AAQ99298/c
ID AAQ99298 standard; cDNA; 20 BP.

XX AC AAQ99298;

XX DT 06-SEP-1996 (first entry)

XX DE Multi-drug resistant-1 gene antisense oligonucleotide 1112.

XX KW Antisense oligonucleotide; nucleotides 1710-1729 and 3639-3658;

XX KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;
XX KW glycoprotein; P170; inhibition; expression; treatment; cancer cells;
XX KW induction; prevention; ss.

XX OS Synthetic.

XX FN WO9602556-A2.

XX PD 01-FEB-1996.

XX PF 18-JUL-1995; 95WO-US009011.

XX PR 18-JUL-1994; 94US-00276567.

XX FA (HYBR-) HYBRIDON INC.

XX PI Smyth AP;

XX DR WPI; 1996-105848/11.

XX PT New oligo:nucleotide(s) complementary to the MDR-1 gene - used for
XX PT preventing induction of multi:drug resistance or for treating multi:drug
XX PT resistant cancer cells.

XX PS Claim 9; Page 14; 43pp; English.

XX CC The present oligonucleotide is antisense to nucleotides 1710-1729 and
XX CC 3639-3658 of the multi-drug resistant-1 (MDR-1) gene, which encode the
XX CC nucleotide binding sites of the plasma membrane glycoprotein, P170. The
XX CC oligonucleotide inhibits the expression of P170, and can therefore be
XX CC used to treat MDR cancer cells, and prevent the induction of MDR in
XX CC cancer cells and the expression of P170 in cells

XX SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 67.4%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGAAGGGGGTGGGTG 17

Db 18 GAGAAGGGGTGCGGTG 3
|||||||

RESULT 27

AAQ99297/c

ID AAQ99297 standard; cDNA; 20 BP.

XX AC AAQ99297;

XX DT 06-SEP-1996 (first entry)

XX DE Multi-drug resistant-1 gene antisense oligonucleotide 1111.

XX KW Antisense oligonucleotide; nucleotides 1709-1729 and 3638-3657;

XX KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;
XX KW glycoprotein; P170; inhibition; expression; treatment; cancer cells;
XX KW induction; prevention; ss.

XX OS Synthetic.

XX FN WO9602556-A2.

XX PD 01-FEB-1996.

XX PF 18-JUL-1995; 95WO-US009011.

XX PR 18-JUL-1994; 94US-00276567.

XX FA (HYBR-) HYBRIDON INC.

XX PI Smyth AP;

XX DR WPI; 1996-105848/11.

XX PT New oligo:nucleotide(s) complementary to the MDR-1 gene - used for
XX PT preventing induction of multi:drug resistance or for treating multi:drug
XX PT resistant cancer cells.

XX PS Claim 8; Page 14; 43pp; English.

XX CC The present oligonucleotide is antisense to nucleotides 1709-1729 and
XX CC 3638-3657 of the multi-drug resistant-1 (MDR-1) gene, which encode the
XX CC nucleotide binding sites of the plasma membrane glycoprotein, P170. The
XX CC oligonucleotide inhibits the expression of P170, and can therefore be
XX CC used to treat MDR cancer cells, and prevent the induction of MDR in
XX CC cancer cells and the expression of P170 in cells

XX SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 67.4%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGAAGGGGGTGGGTG 17
|||||||

Db 17 GAGAAGGGGTGCGGTG 2

RESULT 28

AAQ99296/c

ID AAQ99296 standard; cDNA; 20 BP.

XX AC AAQ99296;

XX DT 06-SEP-1996 (first entry)

XX DE Multi-drug resistant-1 gene antisense oligonucleotide 1110.

XX KW Antisense oligonucleotide; nucleotides 1708-1727 and 3637-3656;

XX KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;
XX KW glycoprotein; P170; inhibition; expression; treatment; cancer cells;
XX KW induction; prevention; ss.

XX OS Synthetic.
XX PN WO9602556-A2.
XX PD 01-FEB-1996.
XX PF 18-JUL-1995; 95WO-US009011.
XX PR 18-JUL-1994; 94US-00276567.
XX PA (HYBR-) HYBRIDON INC.
XX PI Smyth AP;
XX DR WPI; 1996-105848/11.
XX PT New oligo:nucleotide(s) complementary to the MDR-1 gene - used for
PT preventing induction of multi:drug resistance or for treating multi:drug
PT resistant cancer cells.
XX PS Claim 7; Page 14; 43pp; English.
XX CC The present oligonucleotide is antisense to nucleotides 1708-1727 and
CC 3637-3656 of the multi-drug resistant-1 (MDR-1) gene, which encode the
CC nucleotide binding sites of the plasma membrane glycoprotein, P170. The
CC oligonucleotide inhibits the expression of P170, and can therefore be
CC used to treat MDR cancer cells, and prevent the induction of MDR in
CC cancer cells and the expression of P170 in cells
XX Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;
SQ

Query Match 67.4%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GAGAGGGGGTGGGTG 17
Db 16 GAGAGGGGGTGGGTG 1

RESULT 29
AAD48534
ID AAD48534 standard; DNA; 20 BP.
XX AC AAD48534;
XX DT 24-FEB-2003 (first entry)
XX DE Chicken lysozyme gene fragment sequencing PCR primer, lys033for.
XX KW Lysozyme gene expression control region; chromosomal positional effect;
XX KW transgene; avian cell; PCR; primer; chicken; ss.
XX OS Gallus sp.
XX PN WO200279447-A2.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-US009866.
XX PR 30-MAR-2001; 2001US-0280004P.
XX PR 03-AUG-2001; 2001US-00922549.
XX PR 25-JAN-2002; 2002US-0351550P.
XX PA (AVIG-) AVIGENICS INC.
XX PI Rapp JC;
XX DR WPI; 2003-046807/04.
XX PT New isolated or recombinant nucleic acid for reducing the chromosomal

PT positional effect of a transgene, comprises an isolated avian lysozyme
PT gene expression control region.
XX Example 1; Fig 1; 88pp; English.
XX CC The invention relates to an isolated or recombinant nucleic acid or DNA
CC molecule comprising an isolated avian lysozyme gene expression control
CC region operably linked to a nucleic acid insert encoding a polypeptide.
CC The nucleic acid is useful for reducing the chromosomal positional effect
CC of a transgene operably linked to the lysozyme gene expression control
CC region and transfected into a recipient avian cell. The present sequence
CC is a PCR primer used for sequencing chicken lysozyme gene expression
CC control region
XX Sequence 20 BP; 3 A; 0 C; 11 G; 6 T; 0 U; 0 Other;
SQ

Query Match 67.4%; Score 12.8; DB 8; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GAGAGGGGGTGGGTG 17
Db 1 GAGAGGGGGTGGGTG 16

RESULT 30
ACC59333
ID ACC59333 standard; DNA; 20 BP.
XX AC ACC59333;
XX DT 08-SEP-2003 (first entry)
XX DE Human MIZIP coding sequence fragment #5.
XX KW Zinc finger protein; MCH-R; MCH receptor; anorectic; appetite disorder;
KW melanin concentrating hormone receptor interacting protein; gene; db.
XX OS Homo sapiens.
XX PN WO2003042242-A1.
XX PD 22-MAY-2003.
XX PF 13-NOV-2002; 2002WO-EP012714.
XX PR 14-NOV-2001; 2001DE-01055841.
XX PA (UYHA-) UNIV HAMBURG-EPPENDORF.
XX PI Richter D, Baechner D, Kreienkamp H;
XX DR WPI; 2003-468631/44.
XX PT New polynucleotide encoding melanin-concentrating hormone receptor
PT interacting protein, useful for diagnosis of appetite disorders and to
PT screen for appetite regulators.
XX PS Disclosure; Fig 4C; 71pp; German.
XX CC The present invention provides the protein and coding sequences of human
CC melanin concentrating hormone receptor (MCH-R) interacting protein. The
CC sequences can be used in the production of transgenic animals useful for
CC studying appetite disorders and treatments. The present sequence is a
CC coding sequence shown in the exemplification of the invention
XX Sequence 20 BP; 4 A; 2 C; 10 G; 4 T; 0 U; 0 Other;
SQ

Query Match 67.4%; Score 12.8; DB 9; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GAGAGGGGGTGGGTG 17

```
Db          ||||| |||||
            2 GAGAGCAGGTGGTG 17

RESULT 31
ADK23418
ID ADK23418 standard; DNA; 20 BP.
XX
AC ADK23418;
XX
DT 18-NOV-2004 (first entry)
XX
DE Acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide #3495.
XX
KW acyl-coenzyme A synthetase 1; ACS1; diabetes; obesity;
KW metabolic syndrome X; cardiovascular disorder; cancer; infection;
KW inflammation; tumour; antisense; ss.
XX
OS Synthetic.
XX
PN WO2004016749-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025389.
XX
PR 14-AUG-2002; 2002US-0403591P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Ross SA;
XX
DR WPI; 2004-203782/19.
XX
PT New antisense compounds targeted to nucleic acid molecules encoding acyl-
PT coenzyme A synthetase 1 (ACS1), useful for treating diseases or
PT conditions associated with aberrant expression of ACS1, e.g. diabetes,
PT obesity or cancer.
XX
PS Claim 3; SEQ ID NO 3495; 940pp; English.
XX
CC The invention relates to an antisense compound targeted to a nucleic acid
CC molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense
CC compound specifically hybridises with and inhibits the expression of
CC ACS1. The antisense oligonucleotides or compounds are useful for
CC inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for
CC treating diseases or conditions associated with aberrant expression of
CC ACS1, e.g. diabetes, obesity, metabolic syndrome X, cardiovascular
CC disorder or cancer. The antisense compounds are also useful as research
CC reagents and kits, or in diagnostic, therapeutic and prophylactic
CC applications, e.g. to prevent or delay infection, inflammation or tumour
CC formation. The present sequence represents an acyl-coenzyme A synthetase
CC 1, ACS1, antisense oligonucleotide.
XX
SQ Sequence 20 BP; 5 A; 2 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 67.4%; Score 12.8; DB 13; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GAAGGGGGTGGGTGCT 19
    ||||| |||||
Db 1 GAAGGTGGTGGTGTCT 16

RESULT 32
ADK23492
ID ADK23492 standard; DNA; 20 BP.
XX
AC ADK23492;
XX
DT 18-NOV-2004 (first entry)
XX

Acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide #3569.
acyl-coenzyme A synthetase 1; ACS1; diabetes; obesity;
metabolic syndrome X; cardiovascular disorder; cancer; infection;
inflammation; tumour; antisense; ss.
Synthetic.
WO2004016749-A2.
26-FEB-2004.
14-AUG-2003; 2003WO-US025389.
14-AUG-2002; 2002US-0403591P.
(PHAA ) PHARMACIA CORP.
Ross SA;
WPI; 2004-203782/19.
New antisense compounds targeted to nucleic acid molecules encoding acyl-
coenzyme A synthetase 1 (ACS1), useful for treating diseases or
conditions associated with aberrant expression of ACS1, e.g. diabetes,
obesity or cancer.
Claim 3; SEQ ID NO 3569; 940pp; English.
The invention relates to an antisense compound targeted to a nucleic acid
molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense
compound specifically hybridises with and inhibits the expression of
ACS1. The antisense oligonucleotides or compounds are useful for
inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for
treating diseases or conditions associated with aberrant expression of
ACS1, e.g. diabetes, obesity, metabolic syndrome X, cardiovascular
disorder or cancer. The antisense compounds are also useful as research
reagents and kits, or in diagnostic, therapeutic and prophylactic
applications, e.g. to prevent or delay infection, inflammation or tumour
formation. The present sequence represents an acyl-coenzyme A synthetase
1, ACS1, antisense oligonucleotide.
Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 67.4%; Score 12.8; DB 13; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGAAGGGGGTGGGTGC 18
    ||||| |||||
Db 5 AGAAGGTGGTGGTGC 20

RESULT 33
AAQ99295/c
ID AAQ99295 standard; cDNA; 22 BP.
XX
AC AAQ99295;
XX
DT 06-SEP-1996 (first entry)
XX
DE Multi-drug resistant-1 gene antisense oligonucleotide 707.
XX
KW Antisense oligonucleotide; nucleotides 1708-1729 and 3637-3658;
KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;
KW glycoprotein; PL70; inhibition; expression; treatment; cancer cells;
KW induction; prevention; ss.
XX
OS Synthetic.
XX
PN WO9602556-A2.
XX
PD 01-FEB-1996.
```

XX 18-JUL-1995; 95WO-US009011.
 XX
 XX 18-JUL-1994; 94US-00276567.
 XX
 XX (HYBR-) HYBRIDON INC.
 XX
 XX Smyth AP;
 XX
 XX WPI; 1996-105848/11.
 XX
 XX New oligo:nucleotide(s) complementary to the MDR-1 gene - used for
 XX preventing induction of multi:drug resistance or for treating multi:drug
 XX resistant cancer cells.
 XX
 XX Claim 6; Page 14; 43pp; English.
 XX
 XX The present oligonucleotide is antisense to nucleotides 1708-1729 and
 XX 3637-3658 of the multi-drug resistant-1 (MDR-1) gene, which encode the
 XX nucleotide binding sites of the plasma membrane glycoprotein, P170. The
 XX oligonucleotide inhibits the expression of P170, and can therefore be
 XX used to treat MDR cancer cells, and prevent the induction of MDR in
 XX cancer cells and the expression of P170 in cells
 XX
 XX Sequence 22 BP; 3 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
 XX
 XX Query Match 67.4%; Score 12.8; DB 2; Length 22;
 XX Best Local Similarity 87.5%; Pred. No. 5.9e+04;
 XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 2 GAGAGGGGGTGGGTG 17
 XX ||||| |||||
 XX 18 GAGAGGGGTGTCGGTG 3
 XX
 XX RESULT 34
 XX ADY33449
 XX ID ADY33449 standard; DNA; 23 BP.
 XX
 XX AC ADY33449;
 XX
 XX DT 05-MAY-2005 (first entry)
 XX
 XX DE CFTR gene mutation/polymorphism detection primer, SEQ ID 716.
 XX
 XX KW mutation; SNP detection; cystic fibrosis; primer; PCR; ss.
 XX
 XX OS Synthetic.
 XX
 XX PN WO2005016251-A2.
 XX
 XX PD 24-FEB-2005.
 XX
 XX PF 12-JUL-2004; 2004WO-US022376.
 XX
 XX PR 10-JUL-2003; 2003US-0486864P.
 XX
 XX PA (AMBR-) AMERY GENETICS CORP.
 XX
 XX PI Dunlop CLM, Kamescheidt A;
 XX
 XX DR WPI; 2005-182207/19.
 XX
 XX PT Identifying presence/absence of mutation or polymorphism in cystic
 XX fibrosis transmembrane conductance regulator gene, by contacting nucleic
 XX acid and primer set, producing extension product, analyzing product for
 XX mutation or polymorphism.
 XX
 XX PS Claim 1; SEQ ID NO 849; 313pp; English.
 XX
 XX CC The invention relates to a novel method for identifying the
 XX presence/absence of a mutation or polymorphism in the cystic fibrosis
 XX transmembrane conductance regulator (CFTR) gene of subject. The method

XX involves contacting a CFTR nucleic acid from a subject with a primer set
 XX chosen from any one of 553 fully defined 15-100 nt sequences given in
 XX specification, generating an extension product from the primer set having
 XX a mutation or polymorphism, and analyzing the extension product. The
 XX invention further comprises: a method for identifying the presence or
 XX absence of a genetic marker in the cystic fibrosis transmembrane
 XX conductance regulator (CFTR) gene of a subject, which involves providing
 XX a DNA sample from the subject, providing at least one primer set that is
 XX any number between 1-75 nucleotides upstream or downstream of a primer
 XX set described in the specification, contacting the DNA and at least one
 XX primer set, generating an extension product that comprises a region of
 XX DNA that includes the location of the genetic marker, separating the
 XX extension product on a gel, and identifying the presence or absence of
 XX the genetic marker in the subject by analyzing the separation of the
 XX extension product; and the use of at least one primer set described in
 XX the specification to identify the presence or absence of a mutation or
 XX polymorphism on a CFTR gene. The method and primer sets are useful for
 XX identifying the presence or absence of a mutation or polymorphism in the
 XX cystic fibrosis transmembrane conductance regulator gene of a subject.
 XX This polynucleotide sequence represents a primer used in the CFTR gene
 XX mutation/polymorphism detection of the invention.
 XX
 XX Sequence 23 BP; 6 A; 1 C; 10 G; 6 T; 0 U; 0 Other;
 XX
 XX Query Match 67.4%; Score 12.8; DB 14; Length 23;
 XX Best Local Similarity 87.5%; Pred. No. 5.9e+04;
 XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1 GGAGAGGGGGTGGGT 16
 XX ||||| ||||| |||||
 XX 8 GGAGAGGAGGGGTGTGT 23
 XX
 XX RESULT 35
 XX AAV15574/C
 XX ID AAV15574 standard; DNA; 24 BP.
 XX
 XX AC AAV15574;
 XX
 XX DT 22-MAY-1998 (first entry)
 XX
 XX DE Primer for HIV RNA.
 XX
 XX KW Human immunodeficiency virus; HIV; inhibition; replication;
 XX human topoisomerase I; human topo I; treatment; prevention; PCR primer;
 XX ss.
 XX
 XX OS Synthetic.
 XX
 XX PN Human immunodeficiency virus.
 XX
 XX PD WO9744492-A1.
 XX
 XX PF 27-NOV-1997.
 XX
 XX PR 22-MAY-1997; 97WO-US008686.
 XX
 XX PA 23-MAY-1996; 96US-00652074.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX
 XX PI Hall WW, Takahashi H;
 XX
 XX DR WPI; 1998-018542/02.
 XX
 XX PT Inhibiting replication of HIV in cells with topoisomerase I inhibitor -
 XX particularly camptothecin derivative, specifically used with other anti-
 XX HIV agents, also transgenic mice expressing topoisomerase for drug
 XX screening.
 XX
 XX PS Example 7; Page 51; 83pp; English.
 XX
 XX CC The present sequence was used in the development of a novel method for
 XX the inhibition of human immunodeficiency virus (HIV) replication in a

CC cell. The method comprises treating the cell with an agent that
CC interferes with interaction between human topoisomerase I (topo I) and
CC HIV proteins in the cell, useful in the treatment and prevention of HIV
CC infection
XX
SQ Sequence 24 BP; 2 A; 13 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 2; Length 24;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGAGAAGGGGTGGGT 16
Db 16 GGAGGAGGAGTGGGT 1
RESULT 36
ABK51637
ID ABK51637 standard; DNA; 26 BP.
XX
AC ABK51637;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human ABCG5 gene splice junction sequence #7.
XX
KW Human; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol;
KW arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
KW splice junction; ss.
XX
OS Homo sapiens.
XX
FN WO200227016-A2.
XX
PD 04-APR-2002.
XX
PF 25-SEP-2001; 2001WO-US029859.
XX
PR 25-SEP-2000; 2000US-0235268P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (PATE//) PATEL S B.
PA (DEAN//) DEAN M.
XX
PI Patel SB, Dean M;
XX
DR WPI; 2002-416483/44.
XX
PT Novel mammalian ATP-binding cassette gene 5 polypeptide, and the nucleic
PT acid encoding the polypeptide, useful for treating sitosterolemia,
PT arteriosclerosis and heart diseases.
XX
PS Example 1; Page 28; 66pp; English.
XX
CC The present invention relates to a new mammalian ATP-binding cassette
CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a
CC predisposition for developing sitosterolemia, arteriosclerosis or heart
CC disease. The molecules of the invention are also useful for identifying a
CC compound which alters ABCG5 activity level comprising contacting a cell
CC culture or mammal which have ABCG5 polypeptide with a compound and
CC measuring ABCG5 biological activity in the cell culture or in mammal,
CC where an increase or decrease in ABCG5 biological activity compared to
CC ABCG5 biological activity in a control cell culture or mammal not
CC contacted with the compound, identifies a compound that increases or
CC decreases ABCG5 activity respectively. The cell culture or mammal
CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The
CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the
CC polypeptide in a cell culture or mammal is also compared with that of a
CC second cell culture or mammal comprising a wild type ABCG5 polypeptide.
CC Stimulation of ABCG5 activity is useful for treating or preventing
CC hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's
CC disease. The method of the invention is useful for increasing cholesterol
CC excretion and/or decreasing cholesterol adsorption. The present nucleic

CC acid sequence represents one of a collection (ABK51631-ABK51654) of human
CC ABCG5 gene splice junction sequences
XX
SQ Sequence 26 BP; 6 A; 9 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 6; Length 26;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 AGAAGGGGTGGGTGC 18
Db 3 AGAAGAGAGTGGGTGC 18
RESULT 37
ADZ15700
ID ADZ15700 standard; DNA; 26 BP.
XX
AC ADZ15700;
XX
DT 16-JUN-2005 (first entry)
XX
DE Mutagenic PCR primer used to amplify human p53 cDNA - SEQ ID 510.
XX
KW DNA library; DNA microarray; mutagenesis; PCR; primer; ss; p53 gene.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN JP2003265187-A.
XX
PD 24-SEP-2003.
XX
PF 19-MAR-2002; 2002JP-00076990.
XX
PR 19-MAR-2002; 2002JP-00076990.
XX
PA (TOHO-) TOHOKU TECHNOARCH KK.
XX
DR WPI; 2004-183645/18.
XX
PT Constructing a mutant p53 gene library by performing first PCR using
PT oligonucleotide specifying mutation induction as primer, performing
PT second PCR using product of first PCR, as megaprimer and PCR cloning a
PT PCR product in gap repair vector.
XX
PS Claim 8; SEQ ID NO 512; 664pp; Japanese.
XX
CC The invention relates to a novel method for constructing a comprehensive
CC p53 mutant gene library. The method comprises carrying out a first PCR
CC using an oligonucleotide specifying mutation induction as a primer, and
CC then carrying out a second PCR using the PCR product obtained from first
CC PCR as a megaprimer, and cloning the PCR product thus obtained into a gap
CC repair vector. The method of the invention may be useful for constructing
CC a comprehensive p53 mutant gene library. The mutant gene library thus
CC obtained, is useful for preparing nucleic acid arrays and analyzing the
CC p53 gene. The current sequence is that of a mutagenic PCR primer of the
CC invention which was used to amplify, and thus introduce a single mutation
CC into, a human p53 cDNA.
XX
SQ Sequence 26 BP; 3 A; 4 C; 16 G; 3 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 13; Length 26;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 AGAAGGGGTGGGTGC 18
Db 5 AGGAGGGGTGGGTGC 20
RESULT 38
AAI4972/c

```

ID AAX14972 standard; DNA; 27 BP.
XX AC AAX14972;
XX DT 24-MAR-1999 (first entry)
XX DE Triple helix forming nucleotides 1427-1453 of the p53 gene.
XX KW Triple-helix forming region; Triplex formation; DNA detection;
KW KW identification; bacteria; oncogene; virus; ds.
XX OS Homo sapiens.
XX PN US5861244-A.
XX PD 19-JAN-1999.
XX PF 22-DEC-1993; 93US-00173489.
XX PR 29-OCT-1992; 92US-00968436.
XX PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX PI Hepburn AG, Wang C;
XX WPI; 1999-130384/11.
XX AS Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX PS Disclosure; Col 25-26; 168pp; English.
XX CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX SQ Sequence 27 BP; 2 A; 19 C; 0 G; 6 T; 0 U; 0 Other;
XX Query Match 67.4%; Score 12.8; DB 2; Length 27;
XX Best Local Similarity 87.5%; Pred. No. 5.8e+04;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAGAGGGGGTGGGTG 17
DB 17 GAGATGGGGTGGGAG 2
    |||||
RESULT 39
ADXS58930/c
ID ADXS58930 standard; DNA; 29 BP.
XX AC ADXS58930;
XX DT 05-MAY-2005 (first entry)
XX DE Mouse DG239 TaqMan probe.
XX KW Pancreas disease; metabolic disorder; obesity; syndrome x; analgesic;
KW KW antiangiinal; insulin dependent diabetes mellitus;
KW KW non-insulin dependent diabetes; antidiabetic; anorectic; cytostatic;
KW KW antiinflammatory; gene therapy; diagnosis; antisense therapy; DG239;
KW KW probe; ss.
XX OS Mus sp.
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 5' FAM label"
FT modified_base 29
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= 3' TAMRA label"
XX WO2005014029-A2.
XX PN 17-FEB-2005.
XX PD 15-JUL-2004; 2004WO-EP007916.
XX PF 16-JUL-2003; 2003EP-00016171.
XX PR 17-JUL-2003; 2003EP-00016246.
XX PR 22-JUL-2003; 2003EP-00016711.
XX PR 12-AUG-2003; 2003EP-00018326.
XX PA (DEVE-) DEVELOPEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX PI Onichtchouk D;
XX WPI; 2005-152508/16.
XX AS New pharmaceutical composition having a DG008, DG065, DG210 or DG239
PT protein and/or encoding nucleic acid molecule, useful for diagnosing,
PT preventing or treating pancreatic diseases, such as diabetes, obesity and
PT metabolic syndrome.
XX PS Example 3; SEQ ID NO 20; 82pp; English.
XX CC The invention relates to secreted factors referred to as DG008, DG065,
CC DG210 and DG239 ADXS58911-ADXS58918, which are involved in pancreas
CC development, regeneration, and in the regulation of energy homeostasis.
CC These were identified in a screen for secreted factors expressed in
CC developing mammalian (mouse) pancreas. A claimed pharmaceutical
CC composition comprises a DG008, DG065, DG210 or DG239 protein (or
CC functional fragment), a nucleic acid molecule encoding the protein (or
CC functional fragment), and/or an effector/modulator of the protein or
CC nucleic acid. The composition can be used in the manufacture of an agent
CC for detection and/or verifying, for the treatment, alleviation and/or
CC prevention of pancreatic diseases (e.g. diabetes such as insulin
CC dependent diabetes mellitus or non-insulin dependent diabetes mellitus),
CC obesity, metabolic syndrome (syndrome x) and/or other metabolic diseases
CC or dysfunctions. It can also be used for the manufacture of an agent for
CC the modulation of pancreatic development or for the regeneration of
CC pancreatic tissues or cells, particularly pancreatic beta cells, and may
CC be used in vivo or in vitro. The invention also provides a non-human
CC transgenic animal in which expression of DG008, DG065, DG210 or DG239 is
CC increased or reduced, recombinant host cells, a method of identifying a
CC (poly)peptide involved in the regulation of energy homeostasis, and a
CC method of screening for an agent the effects/modulates the activity of
CC DG008, DG065, DG210 or DG239 or its interaction with a binding target.
CC The present sequence is that of a Taqman probe for mouse DG239. This was
CC used in an example from the invention in a quantitative analysis of
CC expression of DG239 nucleic acids in different mouse tissues.
XX SQ Sequence 29 BP; 10 A; 10 C; 5 G; 4 T; 0 U; 0 Other;
XX Query Match 67.4%; Score 12.8; DB 14; Length 29;
XX Best Local Similarity 87.5%; Pred. No. 5.8e+04;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 AGAAGGGGGTGGGTGC 18
DB 20 AGTAGGGGTGGGTGC 5
    |||||

```

RESULT 40
ID ADW28628 standard; DNA; 30 BP.
XX
AC ADW28628;
XX
DT 07-APR-2005 (first entry)
XX
DE HER-2 splice isoform 1 peptide oligonucleotide, SEQ ID 5.
XX
KW Cytostatic; Antirheumatic; Antidiabetic; Cardiant; Nootropic;
KW Neuroprotective; antibody identification; antibody production;
KW antibody therapy; cancer; ss.
XX
OS Homo sapiens.
XX
PN US2005009110-A1.
XX
PD 13-JAN-2005.
XX
PF 08-JUL-2003; 2003US-00615343.
XX
PR 08-JUL-2003; 2003US-00615343.
XX
PA (CHAN/) CHANG X.
XX
PI Chang X;
XX
WPI; 2005-099971/11.
DR P-PSDB; ADW28629.
XX
XX
PT Identifying antibody to protein, involves contacting solid surface coated
PT with antibodies with fusion protein having portion of target protein and
PT carrier protein and conducting assay to determine presence of carrier
PT protein.
XX
PS Example 4; SEQ ID NO 5; 55pp; English.
XX
XX
CC The present invention relates to a method for identifying antibodies for
CC target proteins. The method comprises: (i) contacting an antibody-coated
CC solid surface with a fusion protein, where the antibodies bind
CC specifically to the fusion protein and the fusion protein comprises at
CC least a portion of the target protein linked to a carrier protein, and
CC (ii) conducting an assay to determine the presence of the carrier
CC protein, where the presence of a carrier protein indicates the presence
CC of an antibody to the target protein. The target protein may be an
CC isoform of a protein that is associated with disease, e.g. Vascular
CC Endothelial Growth Factor (VEGF) isoforms VEGF165 (ADW28644) and VEGF121
CC (PSN; ADW28645), which are associated with cancer; Prostate Specific Antigen
CC (PSA; ADW28642), which is associated with prostate cancer and Her2
CC (ADW28640), which is associated with breast cancer. Also claimed are
CC methods for: generating (M2) monoclonal antibodies, where each monoclonal
CC antibody binds to a target protein, specifically at least one monoclonal
CC antibody that binds to an isoform of a protein that is associated with a
CC disease; isolating (M3) an antibody binding specifically to a target
CC protein from several antibodies that are associated with the nucleic
CC acid(s) encoding the antibody; determining (M4) the presence of an
CC antigen in a sample; and identifying (M5) an epitope on a target protein.
CC The antibodies identified by (M1) are useful for treating or preventing
CC diseases in which the presence of an antibody to a particular molecule is
CC beneficial. The antibodies are useful for targeting agents such as toxins
CC to particular cells e.g., cancer cell. (M1) is useful for identifying
CC epitopes on target protein which are used for preparing DNA vaccines
CC having nucleotide sequences encoding epitope of a disease associated
CC protein isoforms used for prevention or treatment of diseases such as
CC cancer, rheumatoid arthritis, diabetes, acute myeloid leukemia (AML),
CC chronic lymphocytic leukemia (CLL), ovarian cancer, prostate cancer,
CC cardiovascular disease, Alzheimer's disease, etc. The antibodies are
CC useful for detecting antigens e.g. in specific cells, tissue or bodily
CC fluids such as serum, or for affinity purification of antigen from
CC recombinant cell culture or natural sources. The present sequence is an
CC oligonucleotide encoding a HER-2 isoform epitope, which can be used to

CC produce a HER-2 isoform fusion protein.
XX
SQ Sequence 30 BP; 6 A; 15 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 14; Length 30;
Best Local Similarity 87.5%; Pred. No. 5.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 AGAAGGGGGTGGGTGC 18
||| ||| ||| ||| ||| |||
Db 23 AGAGGGGAGTGGGTGC 8
RESULT 41
ADP93340
ID ADP93340 standard; RNA; 19 BP.
XX
AC ADF93340;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human TERT transcript target sequence/siNA upper strand, SEQ ID 57.
XX
KW Cytostatic; vasotropic; protozoacide; immunosuppressive; dermatological;
KW neuroprotective; anti-HIV; ophthalmological; antiulcer; antirheumatic;
KW antiarthritic; antiinflammatory; gene therapy; telomerase; human; terc;
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; TERC; TERT; ss.
XX
OS Homo sapiens.
XX
PN WO2003070742-A1.
XX
PD 28-AUG-2003.
XX
PF 11-FEB-2003; 2003WO-US004088.
XX
PR 20-FEB-2002; 2002US-0358580P.
XX
PR 11-MAR-2002; 2002US-0363124P.
XX
PR 06-JUN-2002; 2002US-0386782P.
XX
PR 17-JUL-2002; 2002US-0396600P.
XX
PR 29-AUG-2002; 2002US-0406784P.
XX
PR 05-SEP-2002; 2002US-0408378P.
XX
PR 09-SEP-2002; 2002US-0409233P.
XX
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L;
XX
WPI; 2003-689777/65.
XX
XX
CC New short interfering nucleic acid downregulates expression of the
CC telomerase gene useful e.g. for treatment and diagnosis of cancer.
XX
PS Example 3; SEQ ID NO 57; 145pp; English.
XX
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the one or more telomerase genes by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
CC used to modulate expression of the telomerase genes in cells, tissue

CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
 CC transplants for the treatment of a variety of conditions. They may be
 CC used for treating cancer, restenosis, infectious diseases (specifically
 CC protozoal), transplant rejection, or autoimmune or age-related diseases,
 CC e.g. multiple sclerosis, lupus erythematosus, AIDS, macular degeneration,
 CC skin ulcers and rheumatoid arthritis. The siNAs are also useful for drug
 CC screening, diagnosis, therapeutic target identification and validation,
 CC genetic engineering, pharmacogenomics, studying gene function, and gene
 CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
 CC represents the upper strand of a human TERT-targeted double-stranded
 CC siNA, which is identical to the c-fos transcript target sequence.
 XX
 XX Sequence 19 BP; 1 A; 3 C; 13 G; 0 T; 2 U; 0 Other;
 SQ
 Query Match 66.3%; Score 12.6; DB 10; Length 19;
 Best Local Similarity 68.4%; Pred. No. 7.1e+04;
 Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GGAGAGGGGGTGGTGCT 19
 DB 1 GGAGCGGGCGGUGGGGCT 19
 RESULT 42
 ADF93594/c
 ID ADF93594 standard; RNA; 19 BP.
 XX
 AC ADF93594;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Human TERT siNA lower strand, SEQ ID 321.
 XX
 KW Cytostatic; vasotropic; protozoacide; immunosuppressive; dermatological;
 KW neuroprotective; anti-HIV; ophthalmological; antiulcer; antirheumatic;
 KW antiarthritic; antiinflammatory; gene therapy; telomerase; human; terc;
 KW RNA interference; short interfering nucleic acid; siNA;
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;
 KW drug screening; diagnosis; therapeutic target identification;
 KW pharmacogenomics; gene function analysis; gene mapping; TERC; TERT; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003070742-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 11-FEB-2003; 2003WO-US004088.
 XX
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 17-JUL-2002; 2002US-0396600P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J, Beigelman L;
 XX
 DR WPI; 2003-689777/65.
 XX
 PT New short interfering nucleic acid downregulates expression of the
 PT telomerase gene useful e.g. for treatment and diagnosis of cancer.
 XX
 PS Example 3; SEQ ID NO 321; 145pp; English.
 XX
 CC The invention relates to short interfering nucleic acids (siNA) which
 CC downregulate expression of the one or more telomerase genes by RNA
 CC interference. The siNAs may or may not comprise ribonucleotides and may

CC be double or single stranded. They further comprise sense and antisense
 CC regions, or alternatively are assembled from a sense oligonucleotide and
 CC an antisense oligonucleotide. Specifically, the siNAs include short
 CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
 CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
 CC can contain deoxyribonucleotides, and can be chemically synthesised,
 CC expressed from a vector or enzymatically synthesised. The invention also
 CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
 CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
 CC used to modulate expression of the telomerase genes in cells, tissue
 CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
 CC transplants for the treatment of a variety of conditions. They may be
 CC used for treating cancer, restenosis, infectious diseases (specifically
 CC protozoal), transplant rejection, or autoimmune or age-related diseases,
 CC e.g. multiple sclerosis, lupus erythematosus, AIDS, macular degeneration,
 CC skin ulcers and rheumatoid arthritis. The siNAs are also useful for drug
 CC screening, diagnosis, therapeutic target identification and validation,
 CC genetic engineering, pharmacogenomics, studying gene function, and gene
 CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
 CC represents the lower strand of a human TERT-targeted double-stranded
 CC siNA.
 XX
 XX Sequence 19 BP; 2 A; 13 C; 3 G; 0 T; 1 U; 0 Other;
 SQ
 Query Match 66.3%; Score 12.6; DB 10; Length 19;
 Best Local Similarity 78.9%; Pred. No. 7.1e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GGAGAGGGGGTGGTGCT 19
 DB 19 GGAGCGGGCGTGGGGCT 1
 RESULT 43
 ADF64570
 ID ADF64570 standard; RNA; 19 BP.
 XX
 AC ADF64570;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human G72 siNA oligonucleotide SEQ ID NO:16.
 XX
 KW RNA interference; short interfering nucleic acid; siNA;
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;
 KW drug screening; diagnosis; therapeutic target identification;
 KW pharmacogenomics; gene function analysis; gene mapping; neuroleptic;
 KW schizophrenia; human; G72; target sequence; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003070743-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-US004397.
 XX
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 05-DEC-2002; 2002US-0431105P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J, Beigelman L, Haerberli P;
 XX
 DR WPI; 2003-712607/67.

XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of schizophrenia, downregulates expression of the G72 gene.
XX
XX
XX Example 3; SEQ ID NO 16; 139pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human G72 gene by RNA interference. The
CC siNAs may or may not comprise ribonucleotides and may be double or single
CC stranded. They further comprise sense and antisense regions, or
CC alternatively are assembled from a sense oligonucleotide and an antisense
CC oligonucleotide. Specifically, the siNAs include short interfering RNA
CC (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA
CC (shRNA). The siNAs can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the G72 gene in cells, tissue explants or organisms (e.g.,
CC by ex vivo gene therapy), or in grafts and transplants for the treatment
CC of a variety of conditions. The human G72 siNAs have neuroleptic activity
CC and can be used for treating schizophrenia. The siNAs are also useful for
CC drug screening, diagnosis, therapeutic target identification and
CC validation, genetic engineering, pharmacogenomics, studying gene
CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC The present sequence represents the upper strand of a human G72-targeted
CC double-stranded siNA, which is identical to the G72 transcript target
CC sequence.
XX
SQ Sequence 19 BP; 5 A; 2 C; 8 G; 0 T; 4 U; 0 Other;
Query Match 66.3%; Score 12.6; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.1e+04;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GGAGAAGGGGGTGGTGCT 19
Db 1 GGAAAAGCTGAGGGGUGCU 19
RESULT 44
ADG64626/c
ID ADG64626 standard; RNA; 19 BP.
XX
XX AC ADG64626;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human G72 siNA oligonucleotide SEQ ID NO:72.
XX
XX RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; neuroleptic;
KW schizophrenia; human; G72; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2003070743-A1.
XX
XX 28-AUG-2003.
XX
XX 13-FEB-2003; 2003WO-US004397.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0385782P.
PR 29-AUG-2002; 2002US-0408784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 05-DEC-2002; 2002US-0431105P.
PR

PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Haeberli P;
XX WPI; 2003-712607/67.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of schizophrenia, downregulates expression of the G72 gene.
XX
XX Example 3; SEQ ID NO 72; 139pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human G72 gene by RNA interference. The
CC siNAs may or may not comprise ribonucleotides and may be double or single
CC stranded. They further comprise sense and antisense regions, or
CC alternatively are assembled from a sense oligonucleotide and an antisense
CC oligonucleotide. Specifically, the siNAs include short interfering RNA
CC (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA
CC (shRNA). The siNAs can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the G72 gene in cells, tissue explants or organisms (e.g.,
CC by ex vivo gene therapy), or in grafts and transplants for the treatment
CC of a variety of conditions. The human G72 siNAs have neuroleptic activity
CC and can be used for treating schizophrenia. The siNAs are also useful for
CC drug screening, diagnosis, therapeutic target identification and
CC validation, genetic engineering, pharmacogenomics, studying gene
CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC The present sequence represents the lower strand of a human G72-targeted
CC double-stranded siNA.
XX
SQ Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;
Query Match 65.3%; Score 12.6; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 7.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GGAGAAGGGGGTGGTGCT 19
Db 19 GGAAAAGCTGATGGTGCT 1
RESULT 45
AEB17755/c
ID AEB17755 standard; RNA; 19 BP.
XX
XX AC AEB17755;
XX
XX 25-AUG-2005 (first entry)
XX
XX G72 siRNA molecule complement sequence/target oligo, SEQ ID 72.
KW short interfering RNA; siRNA; G72; RNA interference; gene silencing;
KW neuroleptic; antisense therapy; Amino acid oxidase; schizophrenia; ss.
XX
XX Synthetic.
OS
XX US2005136436-A1.
XX
XX 23-JUN-2005.
XX
XX 19-AUG-2004; 2004US-00923640.
XX
XX 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR


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Qy 1 GGAGAGGGGGTGGTGCT 19
Db 1 GGAAAGCUGAUGGUGCU 19

RESULT 47
AEB15820/c
ID AEB15820 standard; RNA; 19 BP.
AC AEB15820;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human telomerase-targeted siRNA strand SeqID311.
XX
KW RNA interference; gene silencing; short interfering RNA; siRNA;
KW cytosolic; immunosuppressive; vasotropic; antimicrobial; cancer;
KW restenosis; transplant rejection; autoimmune disease; hyperproliferation;
KW aging; drug screening; diagnostic; genetic engineering; gene mapping; ss;
KW telomerase.
XX
OS Homo sapiens.
XX
PN US2005153916-A1.
XX
PD 14-JUL-2005.
XX
PF 20-AUG-2004; 2004US-00923330.
XX
PR 18-MAY-2001; 2001US-0292217P.
XX
PR 20-JUL-2001; 2001US-0306883P.
XX
PR 13-AUG-2001; 2001US-0311865P.
XX
PR 20-FEB-2002; 2002US-0358580P.
XX
PR 06-MAR-2002; 2002US-0362016P.
XX
PR 11-MAR-2002; 2002US-0363124P.
XX
PR 20-MAY-2002; 2002WO-US015876.
XX
PR 06-JUN-2002; 2002US-0386782P.
XX
PR 17-JUL-2002; 2002US-0396600P.
XX
PR 29-AUG-2002; 2002US-0406784P.
XX
PR 05-SEP-2002; 2002US-0408378P.
XX
PR 09-SEP-2002; 2002US-0409293P.
XX
PR 15-JAN-2003; 2003US-0440129P.
XX
PR 11-FEB-2003; 2003WO-US004088.
XX
PR 20-FEB-2003; 2003WO-US005028.
XX
PR 30-APR-2003; 2003US-00444853.
XX
PR 23-MAY-2003; 2003US-00444853.
XX
PR 24-OCT-2003; 2003US-00693059.
XX
PR 24-NOV-2003; 2003US-00720448.
XX
PR 03-DEC-2003; 2003US-00727780.
XX
PR 14-JAN-2004; 2004US-00757803.
XX
PR 10-FEB-2004; 2004US-0543480P.
XX
PR 13-FEB-2004; 2004US-00780447.
XX
PR 16-APR-2004; 2004US-00826966.
XX
PR 30-APR-2004; 2004WO-US013456.
XX
PR 24-MAY-2004; 2004WO-US016390.
XX
XX (STRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L;
XX
XX WPI; 2005-496858/50.
XX
XX Novel chemically synthesized double-stranded short interfering nucleic
XX acid molecule directing cleavage of telomerase RNA by RNA interference,
XX useful for treating cancer and restenosis.
XX
XX Claim 33; SEQ ID NO 311; 304pp; English.
XX
XX The invention relates to chemically synthesized short interfering nucleic
XX acids (siRNAs) which downregulate expression of telomerase genes by RNA
XX interference. The siRNAs may or may not comprise ribonucleotides, can
XX contain deoxyribonucleotides, can be chemically modified and may be
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CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siRNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising an siRNA targeted to the human telomerase mRNA
CC which may have a cytostatic, immunosuppressive, vasotropic or
CC antimicrobial activity. The invention further discloses expression
CC vectors and host cells comprising an siRNA of the invention. The siRNAs are
CC used to modulate expression of the telomerase gene in cells, tissue
CC explants or organisms (for example by ex vivo gene therapy), or in grafts
CC and transplants for the treatment of a variety of conditions. They may be
CC used in the treatment of cancer, restenosis, transplant and/or tissue
CC rejection, and/or autoimmune, proliferative, infectious, and age-related
CC diseases, disorders or conditions. The siRNAs may also be used in drug
CC screening, diagnosis, therapeutic target identification and validation,
CC genetic engineering, pharmacogenomics, studying gene function, and gene
CC mapping (for example of single nucleotide polymorphisms). The present
CC sequence represents the antisense strand of a human telomerase-targeted
CC double-stranded siRNA.
XX
SQ Sequence 19 BP; 2 A; 13 C; 3 G; 0 T; 1 U; 0 Other;
Query Match 66.3%; Score 12.6; DB 14; Length 19;
Best Local Similarity 78.9%; Pred. No. 7.le+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGTGCT 19
Db 19 GGAGCGGGCGTGGGGCT 1

RESULT 48
AEB15597
ID AEB15597 standard; RNA; 19 BP.
AC AEB15597;
XX
XX 22-SEP-2005 (first entry)
XX
DE Human telomerase-targeted siRNA strand SeqID88.
XX
KW RNA interference; gene silencing; short interfering RNA; siRNA;
KW cytosolic; immunosuppressive; vasotropic; antimicrobial; cancer;
KW restenosis; transplant rejection; autoimmune disease; hyperproliferation;
KW aging; drug screening; diagnostic; genetic engineering; gene mapping; ss;
KW telomerase.
XX
OS Homo sapiens.
XX
PN US2005153916-A1.
XX
PD 14-JUL-2005.
XX
PF 20-AUG-2004; 2004US-00923330.
XX
PR 18-MAY-2001; 2001US-0292217P.
XX
PR 20-JUL-2001; 2001US-0306883P.
XX
PR 13-AUG-2001; 2001US-0311865P.
XX
PR 20-FEB-2002; 2002US-0358580P.
XX
PR 06-MAR-2002; 2002US-0362016P.
XX
PR 11-MAR-2002; 2002US-0363124P.
XX
PR 20-MAY-2002; 2002WO-US015876.
XX
PR 06-JUN-2002; 2002US-0386782P.
XX
PR 17-JUL-2002; 2002US-0396600P.
XX
PR 29-AUG-2002; 2002US-0406784P.
XX
PR 05-SEP-2002; 2002US-0408378P.
XX
PR 09-SEP-2002; 2002US-0409293P.
XX
PR 15-JAN-2003; 2003US-0440129P.
XX
PR 11-FEB-2003; 2003WO-US004088.
XX
PR 20-FEB-2003; 2003WO-US005028.
XX
PR 30-APR-2003; 2003US-00444853.
XX
PR 23-MAY-2003; 2003US-00444853.
XX
PR 24-OCT-2003; 2003US-00693059.
XX
PR 24-NOV-2003; 2003US-00720448.
XX
PR 03-DEC-2003; 2003US-00727780.
XX
PR 14-JAN-2004; 2004US-00757803.
XX
PR 10-FEB-2004; 2004US-0543480P.
XX
PR 13-FEB-2004; 2004US-00780447.
XX
PR 16-APR-2004; 2004US-00826966.
XX
PR 30-APR-2004; 2004WO-US013456.
XX
PR 24-MAY-2004; 2004WO-US016390.
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PR 23-MAY-2003; 2003US-00444853.
 PR 23-OCT-2003; 2003US-00693059.
 PR 24-NOV-2003; 2003US-00720448.
 PR 03-DEC-2003; 2003US-00727780.
 PR 14-JAN-2004; 2004US-00757803.
 PR 10-FEB-2004; 2004US-05434808.
 PR 13-FEB-2004; 2004US-00780447.
 PR 16-APR-2004; 2004US-00826966.
 PR 30-APR-2004; 2004US-0013456.
 PR 24-MAY-2004; 2004WO-US016390.
 PA (SIRN-) SIENA THERAPEUTICS INC.
 XX
 XX Mcswiggen J, Beigelman L;
 PI WPI; 2005-496858/50.
 DR
 XX
 PT Novel chemically synthesized double-stranded short interfering nucleic
 PT acid molecule directing cleavage of telomerase RNA by RNA interference,
 PT useful for treating cancer and restenosis.
 XX
 XX Claim 33; SEQ ID NO 88; 304pp; English.
 PS
 CC The invention relates to chemically synthesized short interfering nucleic
 CC acids (siRNAs) which downregulate expression of telomerase genes by RNA
 CC interference. The siRNAs may or may not comprise ribonucleotides, can
 CC contain deoxyribonucleotides, can be chemically modified and may be
 CC double or single stranded. They further comprise sense and antisense
 CC regions, or alternatively are assembled from a sense oligonucleotide and
 CC an antisense oligonucleotide. Specifically, the siRNAs include short
 CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
 CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
 CC compositions comprising a siRNA targeted to the human telomerase mRNA
 CC which may have a cytostatic, immunosuppressive, vasotropic or
 CC antimicrobial activity. The invention further discloses expression
 CC vectors and host cells comprising an siRNA of the invention. The siRNAs are
 CC used to modulate expression of the telomerase gene in cells, tissue
 CC explants or organisms (for example by ex vivo gene therapy), or in grafts
 CC and transplant for the treatment of a variety of conditions. They may be
 CC used in the treatment of cancer, restenosis, transplant and/or tissue
 CC rejection, and/or autoimmune, proliferative, infectious, and age-related
 CC diseases, disorders or conditions. The siRNAs may also be used in drug
 CC screening, diagnosis, therapeutic target identification and validation,
 CC genetic engineering, pharmacogenomics, studying gene function, and gene
 CC mapping (for example of single nucleotide polymorphisms). The present
 CC sequence represents the sense strand of a human telomerase-targeted
 CC double-stranded siRNA, which is identical to the telomerase transcript
 CC target sequence.
 XX
 XX Sequence 19 BP; 1 A; 3 C; 13 G; 0 T; 2 U; 0 Other;
 Query Match 66.3%; Score 12.6; DB 14; Length 19;
 Best Local Similarity 68.4%; Pred. No. 7.1e+04;
 Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GGAGGAGGGGGTGGGTGCT 19
 Db 1 GGAGCGGGCGUGGGGGCU 19
 RESULT 49
 AAC66150/c
 ID AAC66150 standard; cDNA; 23 BP.
 XX
 XX AAC66150;
 AC
 XX
 DT 13-FEB-2001 (first entry)
 DE
 XX 21-hydroxylase intron 2 cDNA fragment SEQ ID 14.
 KW Congenital adrenal hyperplasia; diagnosis; 21-hydroxylase; exon 1;
 XX intron 2; exon 4; HLA class III; human; ss.
 XX

OS Synthetic.
 XX WO200063431-A1.
 PN
 XX 26-OCT-2000.
 PD
 XX 14-APR-2000; 2000WO-KR000347.
 PF
 XX 17-APR-1999; 99KR-00013671.
 PR
 XX (SMSU) SAMSUNG FINE CHEM CO LTD.
 PA
 XX Jin DK;
 PI
 XX WPI; 2000-679607/66.
 DR
 XX
 PT Diagnosing congenital adrenal hyperplasia by attaching fragments of 21-
 PT hydroxylase gene to substrates, amplifying DNA segments containing gene
 PT copies from testis DNA, hybridizing gene and analyzing results.
 XX
 XX Claim 6; Page 42; 46pp; English.
 PS
 CC This invention relates to a method for diagnosing congenital adrenal
 CC hyperplasia. The method comprises attaching fragments of 21-hydroxylase
 CC gene (exon 1, intron 2, exon 4) to substrates, amplifying DNA segments
 CC containing copies of the gene from genomic DNA of testis using PCR,
 CC hybridising the gene with the PCR product and analysing the results of
 CC hybridisation. The steroid 21-hydroxylase gene is located in the HLA
 CC class III gene region on chromosome 6. The method is used for the
 CC diagnosis of congenital hyperplasia. Oligonucleotides AAC66148 - AAC66161
 CC are fragments and antisense oligonucleotides of the 21-hydroxylase gene
 CC (exon 1, intron 2, and exon 4). The 21-hydroxylase gene sequence is
 CC represented in AAC66162, and PCR primers AAC66163 - AAC66172 are used to
 CC amplify exon 1, intron 2, and exon 4 of the 21-hydroxylase gene in
 CC examples illustrating the method of the invention
 XX
 XX Sequence 23 BP; 4 A; 12 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 66.3%; Score 12.6; DB 3; Length 23;
 Best Local Similarity 78.9%; Pred. No. 7.1e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GGAGGAGGGGGTGGGTGCT 19
 Db 23 GCAGGAGGAGGTGGGGGCT 5
 RESULT 50
 AEF42944/c
 ID AEF42944 standard; DNA; 23 BP.
 XX
 XX AEF42944;
 AC
 XX 23-MAR-2006 (first entry)
 DT
 XX Human ABC gene, ABC10, reverse real time RT-PCR primer.
 DE
 XX ABC10; ABC transporter; multi-drug resistance; ss; RT-PCR;
 KW reverse transcriptase PCR; primer; cancer; cytostatic; neoplasm;
 KW drug discovery; ATP-binding cassette; pharmaceutical.
 XX
 XX Homo sapiens.
 OS
 XX WO2006009765-A2.
 PN
 XX 26-JAN-2006.
 PD
 XX 16-JUN-2005; 2005WO-US021253.
 PF
 XX 18-JUN-2004; 2004US-0580397P.
 PR 19-AUG-2004; 2004US-0602640P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA

XX Szakacs G, Annereau J, Lababidi S, Gottesman MM, Weinstein J;
XX WPI; 2006-154816/16.
XX
XX Use of antiproliferative agent having therapeutic activity that is
PT potentiated by ATP-binding cassette transporter protein for inhibiting
PT growth of neoplastic cells during treatment of multi-drug resistance
PT cancer.
XX
XX Example 1; SEQ ID NO 64; 99pp; English.
XX
XX The invention relates to inhibiting (M1) growth of neoplastic cells or
CC development of multidrug resistance phenotype in cancer involving
CC administration of an antiproliferative agent where the antiproliferative
CC effect of the agent is potentiated by an ATP-binding cassette (ABC)
CC transporter protein such as ABCB1 transporter. Also included are
CC identification (M2) of therapeutic compounds having a therapeutic
CC activity that is potentiated by the expression of an ATP-binding cassette
CC (ABC) transporter gene (involving determining the expression level of at
CC least one ABC gene in a panel of cell lines, determining the level of
CC therapeutic activity of at least one test compound on the panel of cell
CC lines and comparing the level of therapeutic activity with the expression
CC level of the ABC gene, where a positive correlation between the level of
CC therapeutic activity and the expression level of the ABC gene identifies
CC the test compound as having an activity that is potentiated by the
CC expression of the ABC gene) and identifying (M3) therapeutic compounds as
CC substrates for ABC transporters (involving carrying out (M2), where a
CC negative correlation between the level of therapeutic activity and the
CC expression level of the ABC gene identifies the test compound as the
CC substrate for the ABC transporter). The antiproliferative agent is
CC hydrazine derivative of formulae given in the specification. The method
CC is useful for inhibiting the development of multidrug resistance
CC phenotype in cancer and for treatment of multi-drug resistant cancer
CC (including colon carcinoma, renal carcinoma, hepatoma, adrenocortical
CC carcinoma, pancreatic carcinoma, breast cancer, ovarian cancer, sarcoma,
CC small cell lung cancer, acute myeloid leukemia, chronic myeloid leukemia,
CC acute lymphoblastic leukemia, non-Hodgkin's lymphoma, B-cell lymphoma,
CC and T-cell lymphoma). The present sequence is a real time RT-PCR primer
CC for a Human ABC gene used to assay expression of the ABC gene in the
CC method of the invention.
XX
XX Sequence 23 BP; 4 A; 11 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 66.3%; Score 12.6; DB 15; Length 23;
Best Local Similarity 78.9%; Fred. No. 7.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 GGAGAGGGGGTGGTGCT 19
Db 23 GGTGAAGGGGCGCGAGCT 5
Search completed: October 14, 2006, 19:40:52
Job time : 353 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

October 14, 2006, 19:38:30 ; Search time 2259 Seconds
(without alignments)
470.326 Million cell updates

Title: US-10-604-926A-4539
Perfect score: 19
Sequence: 1 gaagaaaggaatgaatct 19

Scoring table: IDENTITY NUC

Scoring cubic: IDENTIFICATION
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 56556

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Minimum DB seq length: 0
Maximum DB seq length: 30
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:★

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1:  gb_est1:*
2:  gb_est3:*
3:  gb_est4:*
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9:  gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description		
	score	Match	Length				
C	1	15.4	81.1	28	11	AZ3931146	1M0156004
	2	13.4	70.5	28	11	AZ307952	1M0010124
	3	13.2	69.5	22	1	A1673793	1A1673793
	4	12.8	67.4	25	1	A1586975	1A1586975
	5	12.8	67.4	29	3	BQ590098	1BQ590098
	6	12.6	66.3	20	1	AZ479594	1M0300B22
	7	12.4	65.3	20	11	AZ345548	1M0080D13
	8	12.4	65.3	24	11	AZ486450	1M0314A06
	9	12.2	64.2	22	1	A1000026	1A1000026
	10	12.2	64.2	22	11	AZ752883	1M0045U09
C	11	12.2	64.2	23	11	AZ800080	1M0057122
	12	12.2	64.2	25	11	AZ943422	1M0204P06
	13	12.2	64.2	27	11	AZ362697	1M0107G23
	14	12.2	64.2	26	11	AZ836891	1M0131N22
	15	12.2	64.2	28	1	A1785472	1A1785472
C	16	12.2	64.2	28	11	AZ483923	1M0309A22
	17	12.2	64.2	28	11	AZ774078	1M00003001
	18	12.2	64.2	30	11	AZ624259	1A0505D06
	19	12.2	64.2	30	11	AZ361601	1M0106B01
	20	12.2	64.2	30	11	AZ361601	1M0106B01

C 93	10.8	56.8	30	11	AZ447206	1M0244J07	C 166	10.6	55.8	28	11	AZ640161	1M0501G23
C 94	10.6	55.8	19	11	AZ447198	1M0244A10	167	10.6	55.8	28	11	AZ806290	2M0068C13
C 95	10.6	55.8	19	11	AZ760597	1M0554N21	168	10.6	55.8	28	11	AZ872959	2M0186F03
C 96	10.6	55.8	19	11	AZ962769	1M0231P08	169	10.6	55.8	28	12	CG734031	1119161H0
C 97	10.6	55.8	20	11	AZ512326	1M0357I18	170	10.6	55.8	28	13	CW020469	CG0736 TI
C 98	10.6	55.8	20	11	AZ645269	1M0510B10	171	10.6	55.8	28	14	DX072937	KBF0803C1
C 99	10.6	55.8	20	11	AZ653361	1M0527D04	172	10.6	55.8	29	11	AZ387832	1M0147F23
C 100	10.6	55.8	20	11	AZ659755	1M0537F22	173	10.6	55.8	29	11	AZ423751	1M0203B22
C 101	10.6	55.8	20	11	AZ969440	2M0242O12	174	10.6	55.8	29	11	AZ662736	1M0542C01
C 102	10.6	55.8	21	11	AZ345432	1M0080D07	175	10.6	55.8	29	11	AZ666737	1M0542C01
C 103	10.6	55.8	21	11	AZ476392	1M0295F12	176	10.6	55.8	29	11	AZ780387	2M0017N12
C 104	10.6	55.8	21	11	AZ512534	1M0358B07	177	10.6	55.8	29	13	CZ194796	PSY10543-
C 105	10.6	55.8	21	11	AZ583408	1M0378N23	178	10.6	55.8	29	14	DU832768	KBF05010N1
C 106	10.6	55.8	21	11	AZ653464	1M0527G11	179	10.6	55.8	30	7	BE275232	601122051
C 107	10.6	55.8	21	11	AZ774703	2M0004G14	180	10.6	55.8	30	9	DN988789	ZEBRA 2P
C 108	10.6	55.8	21	11	AZ783943	2M0026F05	181	10.6	55.8	30	11	AZ337154	1M0067B11
C 109	10.6	55.8	21	11	AZ871715	2M0184B13	182	10.6	55.8	30	11	AZ464926	1M0274J04
C 110	10.6	55.8	21	11	AZ969578	2M0242G20	183	10.6	55.8	30	11	AZ468615	1M0281D22
C 111	10.6	55.8	21	11	AZ978432	2M0254G15	184	10.6	55.8	30	11	AZ588957	1M0397B08
C 112	10.6	55.8	21	14	AG188438	1M0511C07	185	10.6	55.8	30	11	AZ650045	1M0520E05
C 113	10.6	55.8	22	1	AI738599	wi3902.x	186	10.6	55.8	30	11	AZ783172	1M0024F08
C 114	10.6	55.8	22	1	AI748552	sb54f11.y	187	10.6	55.8	22	1	AZ833458	2M0115I02
C 115	10.6	55.8	22	11	AZ327083	1M0050D17	188	10.6	55.8	22	1	AZ864315	2M0173P16
C 116	10.6	55.8	22	11	AZ331988	1M0060B11	189	10.6	55.8	30	11	AZ976285	2M0251H09
C 117	10.6	55.8	22	11	AZ607348	1M0429D18	190	10.6	55.8	30	14	DU834752	KBF05015C1
C 118	10.6	55.8	22	11	AZ645874	1M0511C07	191	10.6	55.8	30	14	AL935924	AL935924 Arabidops
C 119	10.6	55.8	22	11	AZ871408	2M0192D07	192	10.4	54.7	19	11	AZ485264	1M0312Q02
C 120	10.6	55.8	22	11	AZ876923	2M0192D07	193	10.4	54.7	22	1	AI566419	tr95c08.x
C 121	10.6	55.8	22	11	AZ967291	2M0238J09	194	10.4	54.7	22	1	AI631347	1M03347 t283C04.x
C 122	10.6	55.8	22	14	DU834523	KBF0501410	195	10.4	54.7	22	11	AZ582417	1M0374N13
C 123	10.6	55.8	22	14	DX076174	KBF0807G0	196	10.4	54.7	22	11	AZ592243	1M0403F05
C 124	10.6	55.8	23	2	BG926069	HNC23-1-E	197	10.4	54.7	26	11	AZ462630	1M0269F08
C 125	10.6	55.8	23	5	CF302431	7LEAF--07	198	10.4	54.7	27	11	AZ439712	1M0230A06
C 126	10.6	55.8	23	11	AZ353803	1M0092O14	199	10.4	54.7	27	11	AZ456814	1M0282G02
C 127	10.6	55.8	23	11	AZ418429	1M0194F02	200	10.4	54.7	28	1	AI037937	ox53a11.x
C 128	10.6	55.8	23	11	AZ581259	1M0369N11	201	10.4	54.7	28	1	AI635783	1M0374N13
C 129	10.6	55.8	23	11	AZ800632	2M0058B17	202	10.4	54.7	29	11	AZ802638	2M0061C08
C 130	10.6	55.8	23	11	AZ968672	2M0241B09	203	10.4	54.7	29	14	AG189105	AG189105 Pan tregl
C 131	10.6	55.8	24	11	AZ331608	1M0059H12	204	10.2	53.7	18	2	BG925569	BG925569 HNC5-1-E2
C 132	10.6	55.8	24	11	AZ346754	1M0082E12	205	10.2	53.7	19	1	AI570374	AI570374 t078f07.x
C 133	10.6	55.8	24	11	AZ640795	1M0503D04	206	10.2	53.7	19	5	CF314442	HD--02-P1
C 134	10.6	55.8	24	11	AZ789161	2M0036A15	207	10.2	53.7	19	11	AZ447197	1M0244A08
C 135	10.6	55.8	24	11	AZ822871	2M0096B05	208	10.2	53.7	19	11	AZ782026	2M0021123
C 136	10.6	55.8	24	11	AZ823931	1M0098F17	209	10.2	53.7	19	11	AZ819494	2M0091110
C 137	10.6	55.8	25	1	AA912548	ol35c01.s	210	10.2	53.7	19	11	AZ822954	2M0096I10
C 138	10.6	55.8	25	11	AZ348233	1M0084G04	211	10.2	53.7	19	11	AZ824929	2M0099P16
C 139	10.6	55.8	25	11	AZ350753	1M0088M20	212	10.2	53.7	19	11	AZ967656	2M0238M09
C 140	10.6	55.8	25	11	AZ510562	1M0355F11	213	10.2	53.7	20	5	CF338875	CF338875 RCL1--03-
C 141	10.6	55.8	25	11	AZ602480	1M0421F16	214	10.2	53.7	20	11	AZ447706	1M0245C06
C 142	10.6	55.8	25	11	AZ780325	2M017N06	215	10.2	53.7	20	11	AZ475834	1M0294N10
C 143	10.6	55.8	25	11	AZ853337	1M0156A04	216	10.2	53.7	20	11	AZ642891	1M0506D12
C 144	10.6	55.8	25	11	AZ873581	2M0187G19	217	10.2	53.7	20	11	AZ772707	1M0583L18
C 145	10.6	55.8	25	12	CG707197	1119001E1	218	10.2	53.7	20	11	AZ833537	2M0115M09
C 146	10.6	55.8	26	4	BX626114	BX626114	219	10.2	53.7	20	11	AZ862316	2M0169F11
C 147	10.6	55.8	26	5	CF309675	ABF--03-P	220	10.2	53.7	20	13	CL660020	PR10135d
C 148	10.6	55.8	26	11	AZ307654	1M0009F22	221	10.2	53.7	20	14	DX081956	KBF08095A2
C 149	10.6	55.8	26	11	AZ363822	1M0109P03	222	10.2	53.7	21	11	AZ589393	1M0398A20
C 150	10.6	55.8	26	11	AZ462959	1M0271G04	223	10.2	53.7	21	11	AZ595941	2M0227C07
C 151	10.6	55.8	26	11	AZ468564	1M0281G10	224	10.2	53.7	21	14	DU835421	KBF05016K0
C 152	10.6	55.8	26	11	AZ810458	2M0076C02	225	10.2	53.7	22	1	AA996014	o826d08.s
C 153	10.6	55.8	26	11	AZ861534	2M0168K19	226	10.2	53.7	22	1	AI055969	ow30h02.s
C 154	10.6	55.8	26	13	CW982257	KBF007C1	227	10.2	53.7	22	13	AZ982662	2M0263J06
C 155	10.6	55.8	27	11	AZ355810	1M0095G10	228	10.2	53.7	22	14	DU835197	KBF05016D0
C 156	10.6	55.8	27	11	AZ416143	1M0193G14	229	10.2	53.7	22	14	TA137G03P	T. brucei
C 157	10.6	55.8	27	11	AZ426894	1M0208P03	230	10.2	53.7	23	1	AM044554	AM044554
C 158	10.6	55.8	27	11	AZ604434	1M0425I18	231	10.2	53.7	23	1	AM075366	AM075366
C 159	10.6	55.8	27	11	AZ649949	1M0519P18	232	10.2	53.7	23	5	CF333152	CF333152 JMT--01-O
C 160	10.6	55.8	27	11	AZ997581	2M0284J09	233	10.2	53.7	23	9	DR064698	DR064698 ip85c02.g
C 161	10.6	55.8	28	1	AI821537	zt38c07.x	234	10.2	53.7	23	11	AZ309863	1M0017P09
C 162	10.6	55.8	28	4	BX629284	BX629284	235	10.2	53.7	23	11	AZ309863	1M0017P09
C 163	10.6	55.8	28	11	AZ403204	1M0170G19	236	10.2	53.7	23	11	AZ488138	1M0318B13
C 164	10.6	55.8	28	11	AZ459967	1M0265D08	237	10.2	53.7	23	11	AZ611718	1M0438B18
C 165	10.6	55.8	28	11	AZ486749	1M0315G02	238	10.2	53.7	23	11	AZ945654	2M0207C10

c 239	10.2	53.7	23	14	DX036713	KB-R035E0	312	10	52.6	21	14	TA71B09Q	AL457696 T. brucei
240	10.2	53.7	23	14	TA173D05P	AL473896 T. brucei	313	10	52.6	22	1	AJ732535	AJ732535
241	10.2	53.7	23	14	TA356F10P	AL497137 T. brucei	314	10	52.6	22	5	CF282319	CF282319
242	10.2	53.7	24	5	CF340367	CF340367 RCLJ--07-	315	10	52.6	22	11	AZ656873	AZ656873
243	10.2	53.7	24	8	CV055483	BNE1120b1	316	10	52.6	22	11	AZ986234	AZ986234
244	10.2	53.7	24	14	TA17B08P	AL474698 T. brucei	c 317	10	52.6	22	5	CF332288	CF332288
c 245	10.2	53.7	25	1	AI363940	AI363940 qw34b12.x	c 318	10	52.6	23	10	DV226161	DV226161
c 246	10.2	53.7	25	1	AI416870	AI416870 sa19b03.x	319	10	52.6	23	11	AZ329120	AZ329120
c 247	10.2	53.7	25	1	AI443365	AI443365 sa31a10.x	c 320	10	52.6	23	11	AZ764532	AZ764532
c 248	10.2	53.7	25	1	AI648460	AI648460 tz56b06.x	321	10	52.6	24	5	CF304020	CF304020
249	10.2	53.7	25	9	DR074081	DR074081 ik95a03.g	322	10	52.6	24	11	AZ387313	AZ387313
c 250	10.2	53.7	25	11	AZ486714	AZ486714 1M0314J19	c 323	10	52.6	24	11	AZ656029	AZ656029
c 251	10.2	53.7	25	11	AZ633243	AZ633243 1M0486K22	324	10	52.6	24	11	AZ806300	AZ806300
252	10.2	53.7	25	11	AZ795708	AZ795708 2M0051M06	325	10	52.6	24	11	AZ844396	AZ844396
253	10.2	53.7	25	11	AZ810919	AZ810919 2M0076K16	326	10	52.6	24	14	TA363E08P	TA363E08P
c 254	10.2	53.7	25	11	AZ820085	AZ820085 2M0092001	c 327	10	52.6	25	1	AM046161	AM046161
255	10.2	53.7	25	11	AZ950326	AZ950326 2M0214B22	328	10	52.6	25	11	AZ646830	AZ646830
256	10.2	53.7	25	11	AZ997733	AZ997733 2M0284E22	329	10	52.6	25	13	CZ918376	CZ918376
257	10.2	53.7	25	13	CZ908046	CZ908046 4018001F0	c 330	10	52.6	26	1	AJ661750	AJ661750
258	10.2	53.7	25	13	CL681025	CL681025 PR10130a	331	10	52.6	26	2	BN397648	BN397648
c 259	10.2	53.7	25	14	DX055363	DX055363 KB-R05900	332	10	52.6	26	11	AZ767933	AZ767933
c 260	10.2	53.7	25	14	AG191246	AG191246 Pan trolg	333	10	52.6	26	14	DU753579	DU753579
261	10.2	53.7	25	14	TA233G09Q	AL481789 T. brucei	334	10	52.6	27	2	BM395101	BM395101
c 262	10.2	53.7	25	14	TA236H10Q	AL481372 T. brucei	c 335	10	52.6	27	11	AZ453355	AZ453355
c 263	10.2	53.7	25	14	TA261B03P	AL484466 T. brucei	c 336	10	52.6	27	11	AZ473702	AZ473702
c 264	10.2	53.7	26	1	AL588210	AL588210 AL588210	337	10	52.6	27	11	AZ473702	AZ473702
c 265	10.2	53.7	26	11	AZ431644	AZ431644 1M0216L12	c 338	10	52.6	27	14	DU829541	DU829541
c 266	10.2	53.7	26	11	AZ447254	AZ447254 1M0244O20	c 339	10	52.6	28	1	AI351154	AI351154
c 267	10.2	53.7	26	11	AZ864944	AZ864944 2M0174M17	c 340	10	52.6	28	1	AI445347	AI445347
c 268	10.2	53.7	26	13	CL659570	CL659570 PR10134C	341	10	52.6	28	1	AI597957	AI597957
269	10.2	53.7	26	14	DX045718	DX045718 KB-R047B2	c 342	10	52.6	28	1	AJ694147	AJ694147
c 270	10.2	53.7	26	14	TA319G03Q	AL492820 T. brucei	c 343	10	52.6	28	11	AZ345466	AZ345466
271	10.2	53.7	27	11	AZ453223	AZ453223 1M0079M16	344	10	52.6	28	11	AZ614443	AZ614443
272	10.2	53.7	27	11	AZ495213	AZ495213 1M0331A04	c 345	10	52.6	28	11	AZ785207	AZ785207
273	10.2	53.7	27	11	AZ765547	AZ765547 1M0562L21	346	10	52.6	29	11	AZ764536	AZ764536
274	10.2	53.7	27	14	TA286G07Q	AL486597 T. brucei	347	10	52.6	29	11	AZ799171	AZ799171
275	10.2	53.7	28	1	AI783508	AI783508 tz36c05.x	c 348	10	52.6	29	11	AZ833672	AZ833672
c 276	10.2	53.7	28	11	AZ309062	AZ309062 1M0012E14	c 349	10	52.6	30	14	DU829541	DU829541
277	10.2	53.7	28	11	AZ363489	AZ363489 1M0109I06	c 350	10	52.6	30	14	AZ864869	AZ864869
278	10.2	53.7	28	11	AZ649613	AZ649613 1M0519H18	c 351	10	52.6	30	14	DU767213	DU767213
279	10.2	53.7	28	11	AZ792783	AZ792783 2M0045C01	c 352	10	52.6	30	14	TA28A09P	TA28A09P
280	10.2	53.7	28	11	AZ937148	AZ937148 2M0195A18	c 353	9.8	51.6	15	1	AI209036	AI209036
281	10.2	53.7	28	11	AZ957207	AZ957207 2M0224E04	c 354	9.8	51.6	17	1	AJ666397	AJ666397
282	10.2	53.7	28	11	AZ986927	AZ986927 2M0269N13	c 355	9.8	51.6	19	1	AI431460	AI431460
c 283	10.2	53.7	28	12	CC865975	CC865975 SALK 1480	c 356	9.8	51.6	19	5	CF298891	CF298891
284	10.2	53.7	28	13	CL663977	CL663977 PR10145d	c 357	9.8	51.6	19	5	AZ597219	AZ597219
285	10.2	53.7	28	13	CL686485	CL686485 PR10144b	c 358	9.8	51.6	19	11	AZ775541	AZ775541
286	10.2	53.7	28	14	TA186G09P	AL475729 T. brucei	359	9.8	51.6	19	11	AZ949434	AZ949434
287	10.2	53.7	28	14	TA37A10P	AL453013 T. brucei	c 360	9.8	51.6	20	11	AZ465909	AZ465909
288	10.2	53.7	29	5	CF309854	CF309854 ABF--04-D	c 361	9.8	51.6	20	11	AZ619034	AZ619034
289	10.2	53.7	29	11	AZ453011	AZ453011 1M0254J12	362	9.8	51.6	20	11	AZ785534	AZ785534
290	10.2	53.7	29	11	AZ949281	AZ949281 2M0212M12	363	9.8	51.6	20	11	AZ846437	AZ846437
c 291	10.2	53.7	29	11	AZ992478	AZ992478 2M0277H07	364	9.8	51.6	20	11	AZ864576	AZ864576
292	10.2	53.7	29	13	CL660119	CL660119 PR10136b	c 365	9.8	51.6	20	11	AZ957966	AZ957966
293	10.2	53.7	30	1	AM047980	AM047980	c 366	9.8	51.6	21	1	AJ692277	AJ692277
c 294	10.2	53.7	30	1	BQ590438	BQ590438 E012839-0	c 367	9.8	51.6	21	11	AZ387199	AZ387199
c 295	10.2	53.7	30	11	AZ463319	AZ463319 1M0272M03	368	9.8	51.6	21	11	AZ442444	AZ442444
c 296	10.2	53.7	30	11	AZ501729	AZ501729 1M0340N09	c 369	9.8	51.6	21	11	AZ657586	AZ657586
297	10.2	53.7	30	11	AZ633504	AZ633504 1M0488K13	370	9.8	51.6	21	11	AZ856540	AZ856540
298	10.2	53.7	30	11	AZ634665	AZ634665 1M0490P02	371	9.8	51.6	21	11	AZ861360	AZ861360
299	10.2	53.7	30	11	AZ779367	AZ779367 2M0015N07	372	9.8	51.6	21	13	CL669293	CL669293
c 300	10.2	53.7	30	14	DX062633	DX062633 KB-R069I2	373	9.8	51.6	22	1	AA931067	AA931067
c 301	10.2	53.7	30	14	AZ345894	AZ345894 1M0080C24	374	9.8	51.6	22	1	AA1274595	AA1274595
c 302	10.2	53.7	30	14	AZ489350	AZ489350 1M0321K14	375	9.8	51.6	22	1	AI608652	AI608652
c 303	10.2	53.7	30	14	AZ813861	AZ813861 2M0081A01	376	9.8	51.6	22	11	AZ828663	AZ828663
304	10.2	53.7	30	14	AZ861832	AZ861832 2M0168H21	377	9.8	51.6	22	11	AZ837879	AZ837879
c 305	10.2	53.7	30	14	AZ417235	AZ417235 1M0192N15	c 378	9.8	51.6	22	14	DX080981	DX080981
c 306	10.2	53.7	30	14	AZ775620	AZ775620 2M0008D02	379	9.8	51.6	22	14	TA245E10P	TA245E10P
307	10.2	53.7	30	14	AZ782314	AZ782314 2M0022D03	380	9.8	51.6	23	11	AZ305188	AZ305188
308	10.2	53.7	30	14	AZ345794	AZ345794 1M0080H08	c 381	9.8	51.6	23	11	AZ615086	AZ615086
309	10.2	53.7	30	14	AZ451384	AZ451384 1M0250D13	c 382	9.8	51.6	23	11	AZ818371	AZ818371
c 310	10.2	53.7	30	14	AZ819539	AZ819539 2M0091A17	383	9.8	51.6	23	11	AZ819376	AZ819376
c 311	10.2	53.7	30	14	TA368C05Q	AL494597 T. brucei	384	9.8	51.6	23	11	AZ965976	AZ965976

C 385	9.8	51.6	23	14	DX018712	DX018712 KBrB011J1	458	9.6	50.5	22	3	BQ585098	BQ585098 E011826-0
C 386	9.8	51.6	23	14	DX060572	DX060572 KBrB066N1	459	9.6	50.5	22	5	CF281903	CF281903 14ETL--09
C 387	9.8	51.6	23	14	CT010976	CT010976 KBrH118E1	460	9.6	50.5	22	11	AZ307488	AZ307488 1M0009B13
C 388	9.8	51.6	24	5	CF295238	CF295238 3DGS--05	C 461	9.6	50.5	22	11	AZ589449	AZ589449 1M0398M24
C 389	9.8	51.6	24	14	TA155F12Q	TA155F12Q T. brucei	462	9.6	50.5	22	11	AZ603158	AZ603158 1M0422L13
C 390	9.8	51.6	24	14	TA185C06P	TA185C06P T. brucei	463	9.6	50.5	22	11	AZ606880	AZ606880 1M0429H03
C 391	9.8	51.6	24	14	TA235H03Q	TA235H03Q T. brucei	C 464	9.6	50.5	22	11	AZ779122	AZ779122 2M0015M03
C 392	9.8	51.6	25	1	A1041825	A1041825 oy34b05.x	465	9.6	50.5	22	13	CL655007	CL655007 PR10122A
C 393	9.8	51.6	25	1	A1453394	A1453394 t3j7g02.x	466	9.6	50.5	23	11	AZ374746	AZ374746 1M0127D15
C 394	9.8	51.6	25	1	A1471676	A1471676 t19pd02.x	467	9.6	50.5	23	11	AZ410218	AZ410218 1M0182F23
C 395	9.8	51.6	25	1	A1682835	A1682835 wc66h10.x	C 468	9.6	50.5	23	11	AZ439451	AZ439451 1M0230C09
C 396	9.8	51.6	25	1	A1915575	A1915575 tr40g09.x	469	9.6	50.5	23	11	AZ647047	AZ647047 1M0513B22
C 397	9.8	51.6	25	11	AZ450283	AZ450283 1M0249002	C 470	9.6	50.5	23	11	AZ659712	AZ659712 1M0537J18
C 398	9.8	51.6	25	11	AZ500456	AZ500456 1M0338017	C 471	9.6	50.5	23	11	AZ855661	AZ855661 2M0159J17
C 399	9.8	51.6	25	11	AZ6511099	AZ6511099 1M0436K13	C 472	9.6	50.5	23	11	AZ949214	AZ949214 2M0212005
C 400	9.8	51.6	25	11	AZ945526	AZ945526 2M0206L22	473	9.6	50.5	23	11	AZ971749	AZ971749 2M0245C21
C 401	9.8	51.6	25	13	CZ918500	CZ918500 4021009F1	474	9.6	50.5	24	1	AJ668266	AJ668266 AJ568266
C 402	9.8	51.6	25	14	DX046122	DX046122 KBrB047K1	C 475	9.6	50.5	24	5	CF326142	CF326142 JMW11--05-
C 403	9.8	51.6	26	11	AZ424207	AZ424207 1M0203N07	476	9.6	50.5	24	11	AZ845302	AZ845302 2M0145I06
C 404	9.8	51.6	26	11	AZ481118	AZ481118 1M0245C10	477	9.6	50.5	25	1	A1467995	A1467995 t394e07.x
C 405	9.8	51.6	26	11	AZ512846	AZ512846 1M0358N07	C 478	9.6	50.5	25	1	A1571526	A1571526 tr85C03.x
C 406	9.8	51.6	26	11	AZ641136	AZ641136 1M0503E01	C 479	9.6	50.5	25	11	AZ406180	AZ406180 1M0175M18
C 407	9.8	51.6	26	13	CZ919340	CZ919340 4021012G0	480	9.6	50.5	25	11	AZ431597	AZ431597 1M0216C10
C 408	9.8	51.6	26	14	DU831494	DU831494 KBrS008J0	481	9.6	50.5	25	11	AZ438688	AZ438688 1M0228H19
C 409	9.8	51.6	26	14	AJ840729	AJ840729 Arabidops	482	9.6	50.5	25	11	AZ620217	AZ620217 1M0452B23
C 410	9.8	51.6	26	14	TA97C06P	TA97C06P T. brucei	483	9.6	50.5	25	11	AZ776699	AZ776699 2M0010L02
C 411	9.8	51.6	27	9	D17088	D17088 D17088 Kise	C 484	9.6	50.5	25	11	AZ796046	AZ796046 2M0051B17
C 412	9.8	51.6	27	11	AZ948983	AZ948983 2M0212C15	485	9.6	50.5	25	11	AZ937578	AZ937578 2M0195L17
C 413	9.8	51.6	27	11	AZ970595	AZ970595 2M0243I18	486	9.6	50.5	25	13	CL685316	CL685316 PR10140D
C 414	9.8	51.6	27	14	CT014304	CT014304 KBrH122P2	487	9.6	50.5	25	14	TA185B02Q	TA185B02Q T. brucei
C 415	9.8	51.6	27	14	TA356E04P	TA356E04P T. brucei	488	9.6	50.5	25	14	TA356H06P	TA356H06P T. brucei
C 416	9.8	51.6	28	1	A8660464	A8660464 aj85a02.s	489	9.6	50.5	26	11	AZ955924	AZ955924 2M0222P10
C 417	9.8	51.6	28	1	A9554651	A9554651 om95b06.s	C 490	9.6	50.5	26	14	DU833380	DU833380 KBrS012A0
C 418	9.8	51.6	28	1	A1087295	A1087295 oz77h02.x	491	9.6	50.5	26	14	AG190159	AG190159 Pan trogl
C 419	9.8	51.6	28	1	A1174332	A1174332 anl7d02.s	492	9.6	50.5	27	1	AJ649606	AJ649606 AJ549606
C 420	9.8	51.6	28	1	A1306628	A1306628 qn45h01.x	C 493	9.6	50.5	27	1	BM399490	BM399490 50059022
C 421	9.8	51.6	28	1	A1357341	A1357341 qy12e10.x	494	9.6	50.5	27	2	BM399490	BM399490 50059022
C 422	9.8	51.6	28	1	A1446622	A1446622 t325d04.x	495	9.6	50.5	27	5	CD530450	CD530450 06F11 Ara
C 423	9.8	51.6	28	1	A1499167	A1499167 t005h03.x	496	9.6	50.5	27	11	AZ506426	AZ506426 1M0347M04
C 424	9.8	51.6	28	1	A1667101	A1667101 fc37f08.x	497	9.6	50.5	27	11	AZ622014	AZ622014 1M0455I03
C 425	9.8	51.6	28	1	A1745328	A1745328 tr21901.x	498	9.6	50.5	27	11	AZ835935	AZ835935 2M0130K19
C 426	9.8	51.6	28	11	AZ802448	AZ802448 2M0061B20	C 499	9.6	50.5	27	11	AZ979506	AZ979506 2M0256A13
C 427	9.8	51.6	28	11	AZ853408	AZ853408 2M0156P01	500	9.6	50.5	27	12	CG713231	CG713231 1119031A0
C 428	9.8	51.6	29	1	AM075309	AM075309 AM075309	501	9.6	50.5	27	13	CL660039	CL660039 PR10136A
C 429	9.8	51.6	29	11	AZ391891	AZ391891 1M0154F14	C 502	9.6	50.5	27	14	CT021050	CT021050 KBrH131I1
C 430	9.8	51.6	29	11	AZ432529	AZ432529 1M0218C04	503	9.6	50.5	27	14	TA287F07P	TA287F07P T. brucei
C 431	9.8	51.6	29	11	AZ777445	AZ777445 2M0011C19	504	9.6	50.5	28	1	A1628556	A1628556 cy95d11.x
C 432	9.8	51.6	29	11	AZ801486	AZ801486 2M0059P23	C 505	9.6	50.5	28	1	A1687742	A1687742 tp93h01.x
C 433	9.8	51.6	29	11	AZ862317	AZ862317 2M0169J13	C 506	9.6	50.5	28	1	A1918417	A1918417 tr96d10.x
C 434	9.8	51.6	29	12	CG769372	CG769372 TCB52.3.A	C 507	9.6	50.5	28	13	CW982427	CW982427 KBrH007G1
C 435	9.8	51.6	29	13	CZ907899	CZ907899 4018001A0	C 508	9.6	50.5	28	13	CW982427	CW982427 KBrH007G1
C 436	9.8	51.6	29	14	DU829331	DU829331 KBrS004L1	C 509	9.6	50.5	28	13	CZ907021	CZ907021 4011004G0
C 437	9.8	51.6	29	14	TA239G06Q	TA239G06Q T. brucei	C 510	9.6	50.5	29	1	AJ673541	AJ673541 AJ5673541
C 438	9.8	51.6	30	11	AZ406515	AZ406515 1M0175I14	C 511	9.6	50.5	29	5	CJ054334	CJ054334 CJ054334
C 439	9.8	51.6	30	11	AZ787677	AZ787677 2M0034H17	C 512	9.6	50.5	29	11	DN953812	DN953812 it64g12.9
C 440	9.8	51.6	30	13	CZ913610	CZ913610 4013003D0	513	9.6	50.5	29	11	AZ321120	AZ321120 1M0041H16
C 441	9.8	51.6	30	14	DX080575	DX080575 KBrB093C1	514	9.6	50.5	29	11	AZ602874	AZ602874 1M0421B21
C 442	9.8	51.6	30	14	TA183B05P	TA183B05P T. brucei	515	9.6	50.5	29	11	AZ641783	AZ641783 1M0504E06
C 443	9.8	51.6	30	14	TA211H11Q	TA211H11Q T. brucei	C 516	9.6	50.5	29	11	AZ956998	AZ956998 2M0223P12
C 444	9.6	50.5	19	1	A1537209	A1537209 tp06f07.x	C 517	9.6	50.5	29	14	DU835009	DU835009 KBrS015M0
C 445	9.6	50.5	19	1	A1690354	A1690354 tx14f06.x	518	9.6	50.5	29	14	DX056930	DX056930 KBrB062A0
C 446	9.6	50.5	19	1	A1807936	A1807936 wf52e09.x	519	9.6	50.5	30	1	CW999848	CW999848 iv53e08.9
C 447	9.6	50.5	19	11	AZ654214	AZ654214 1M0528H13	520	9.6	50.5	30	11	AZ408503	AZ408503 1M0179P12
C 448	9.6	50.5	20	8	CN752083	CN752083 APhL3SD-X	521	9.6	50.5	30	11	AZ604126	AZ604126 1M0423O13
C 449	9.6	50.5	20	11	AZ627848	AZ627848 1M0474G14	522	9.6	50.5	30	13	CZ558878	CZ558878 M0051780
C 450	9.6	50.5	20	11	AZ818394	AZ818394 2M0008G23	523	9.6	50.5	30	13	CZ559054	CZ559054 M0053020
C 451	9.6	50.5	20	14	DU834060	DU834060 KBrS013F1	C 524	9.6	50.5	30	13	CZ919131	CZ919131 402101H1
C 452	9.6	50.5	20	14	DX030114	DX030114 KBrB026I1	C 525	9.6	50.5	30	14	DU833917	DU833917 KBrS031A1
C 453	9.6	50.5	21	4	BX568462	BX568462 BX568462	C 526	9.6	50.5	30	14	DX063780	DX063780 KBrB071A2
C 454	9.6	50.5	21	11	AZ443821	AZ443821 1M0238I07	527	9.4	49.5	16	1	AA968729	AA968729 or69h11.s
C 455	9.6	50.5	21	11	AZ472401	AZ472401 1M0287C07	C 528	9.4	49.5	16	1	A1684114	A1684114 tx79d02.x
C 456	9.6	50.5	21	14	AG190497	AG190497 Pan trogl	529	9.4	49.5	19	1	AA909236	AA909236 o10a811.s
C 457	9.6	50.5	22	1	A1707945	A1707945 as34g10.x	C 530	9.4	49.5	19	1	A1364573	A1364573 qw37903.x

C 531	9.4	49.5	19	9	DR107492	DR107492 JHU140E12	604	9.4	49.5	26	11	AZ588958	AZ588958 1M0397B09
532	9.4	49.5	19	11	AZ314511	AZ314511 1M0031B20	605	9.4	49.5	26	13	CZ914182	CZ914182 401300SH0
533	9.4	49.5	19	11	AZ326174	AZ326174 1M0048A07	C 606	9.4	49.5	26	14	AI919430	AI919430 Pan trogl
534	9.4	49.5	19	11	AZ369361	AZ369361 1M0119123	C 607	9.4	49.5	26	14	AJ599130	AJ599130 Arabidops
535	9.4	49.5	19	11	AZ381798	AZ381798 1M0138G01	C 608	9.4	49.5	27	8	CX009757	CX009757 io42e08.b
536	9.4	49.5	19	11	AZ4330028	AZ4330028 1M0214116	C 609	9.4	49.5	27	11	AZ403394	AZ403394 1M0171109
537	9.4	49.5	19	11	AZ447936	AZ447936 1M0245018	C 610	9.4	49.5	27	11	AZ479687	AZ479687 1M0300H02
538	9.4	49.5	19	11	AZ453412	AZ453412 1M0254110	C 611	9.4	49.5	27	11	AZ768325	AZ768325 1M0568F17
539	9.4	49.5	19	11	AZ586752	AZ586752 1M0392N24	C 612	9.4	49.5	27	11	AZ840204	AZ840204 2M0136H08
540	9.4	49.5	19	11	AZ644418	AZ644418 1M0508B20	C 613	9.4	49.5	27	11	AZ840194	AZ840194 2M0216004
541	9.4	49.5	19	11	AZ780591	AZ780591 2M0018B09	C 614	9.4	49.5	28	1	AA864806	AA864806 oh02h06.s
542	9.4	49.5	19	11	AZ808178	AZ808178 2M0071A15	C 615	9.4	49.5	28	1	AA886956	AA886956 oi14e09.s
543	9.4	49.5	20	8	CX013532	CX013532 io65g08.b	C 616	9.4	49.5	28	1	AA905471	AA905471 ok01f11.s
544	9.4	49.5	20	9	DZ00001	DZ00001 HUMG00971	C 617	9.4	49.5	28	1	AA911003	AA911003 ok57f12.s
545	9.4	49.5	20	11	AZ368205	AZ368205 1M0118L07	C 618	9.4	49.5	28	1	AI355566	AI355566 qt75g02.x
546	9.4	49.5	20	11	AZ464846	AZ464846 1M0281G04	C 619	9.4	49.5	28	1	AI377008	AI377008 tc34h10.x
547	9.4	49.5	20	11	AZ492477	AZ492477 1M0326D12	C 620	9.4	49.5	28	1	AI529170	AI529170 ui66b12.y
548	9.4	49.5	20	14	AG189827	AG189827 Pan trogl	C 621	9.4	49.5	28	1	AI613531	AI613531 tw22h06.x
549	9.4	49.5	21	11	AZ313243	AZ313243 1M0029H16	C 622	9.4	49.5	28	1	AI623372	AI623372 tw18e04.x
550	9.4	49.5	21	11	AZ660221	AZ660221 1M0538M09	C 623	9.4	49.5	28	1	AI633014	AI633014 tz33d07.x
551	9.4	49.5	21	11	AZ792515	AZ792515 2M0045H04	C 624	9.4	49.5	28	1	AI687017	AI687017 tp81h11.x
552	9.4	49.5	21	11	AZ834643	AZ834643 2M0117N24	C 625	9.4	49.5	28	1	AJ682978	AJ682978 AJ682978
553	9.4	49.5	21	14	AG203513	AG203513 Pan trogl	C 626	9.4	49.5	28	1	AM048443	AM048443
554	9.4	49.5	22	1	AI183338	AI183338 qd41a12.x	C 627	9.4	49.5	28	11	AZ342196	AZ342196 1M0075F07
555	9.4	49.5	22	1	AI721471	AI721471 fc28b01.x	C 628	9.4	49.5	28	11	AZ430095	AZ430095 1M0214U19
556	9.4	49.5	22	11	AZ314354	AZ314354 1M0031B07	C 629	9.4	49.5	28	11	AZ659656	AZ659656 1M0537K08
557	9.4	49.5	22	11	AZ766712	AZ766712 1M0564A03	C 630	9.4	49.5	28	11	AZ828724	AZ828724 2M0105E24
558	9.4	49.5	22	11	AZ769521	AZ769521 1M0570O18	C 631	9.4	49.5	28	11	AZ833779	AZ833779 2M0116A09
559	9.4	49.5	22	11	AZ785902	AZ785902 2M0190K12	C 632	9.4	49.5	28	14	AG192430	AG192430 Pan trogl
560	9.4	49.5	22	11	AZ991498	AZ991498 2M0275C14	C 633	9.4	49.5	29	11	AZ313334	AZ313334 1M0029D03
561	9.4	49.5	22	11	AZ994320	AZ994320 2M0279D17	C 634	9.4	49.5	29	11	AZ479604	AZ479604 1M0300E21
562	9.4	49.5	22	13	CL684513	CL684513 PR10139d	C 635	9.4	49.5	29	11	AZ659788	AZ659788 1M0537O24
563	9.4	49.5	22	14	DU753637	DU753637 ASNF3267	C 636	9.4	49.5	29	11	AZ786433	AZ786433 2M0031M21
564	9.4	49.5	23	1	AJ658745	AJ658745 AJ658745	C 637	9.4	49.5	29	11	AZ795441	AZ795441 2M0049K12
565	9.4	49.5	23	1	AM111999	AM111999 AM111999	C 638	9.4	49.5	29	14	DU835101	DU835101 KB7S016A0
566	9.4	49.5	23	11	AZ310681	AZ310681 1M0025F13	C 639	9.4	49.5	30	9	DZ5861	DZ5861 HUMG04239
567	9.4	49.5	23	11	AZ333226	AZ333226 1M0062F12	C 640	9.4	49.5	30	11	AZ375563	AZ375563 1M0128B24
568	9.4	49.5	23	11	AZ339656	AZ339656 1M0071A14	C 641	9.4	49.5	30	11	AZ995340	AZ995340 2M0281E11
569	9.4	49.5	23	11	AZ653869	AZ653869 1M0527D14	C 642	9.4	49.5	30	13	CZ480720	CZ480720 eo2954-5p
570	9.4	49.5	23	11	AZ793326	AZ793326 2M0046B04	C 643	9.4	49.5	30	14	TA172F01Q	TA172F01Q T. brucei
571	9.4	49.5	23	11	AZ970753	AZ970753 2M0244E01	C 644	9.4	49.5	16	1	AI564678	AI564678 tq78g03.x
572	9.4	49.5	24	1	AJ685589	AJ685589 AJ685589	C 645	9.2	48.4	18	14	DU642495	DU642495 Ciuffi-HI
573	9.4	49.5	24	1	AU260297	AU260297 AU260297	C 646	9.2	48.4	18	14	DU642844	DU642844 Ciuffi-HI
574	9.4	49.5	24	11	AZ404465	AZ404465 1M0172P09	C 647	9.2	48.4	19	1	AI758301	AI758301 ty06a07.x
575	9.4	49.5	24	11	AZ583540	AZ583540 1M0378G01	C 648	9.2	48.4	19	1	AI811474	AI811474 tw43c04.x
576	9.4	49.5	24	11	AZ585617	AZ585617 1M0390123	C 649	9.2	48.4	19	11	AZ343228	AZ343228 1M0076M05
577	9.4	49.5	24	11	AZ773781	AZ773781 2M0001E05	C 650	9.2	48.4	19	11	AZ512762	AZ512762 1M0358M04
578	9.4	49.5	24	11	AZ814317	AZ814317 2M0084C12	C 651	9.2	48.4	19	11	AZ646713	AZ646713 1M0512D20
579	9.4	49.5	24	11	AZ939258	AZ939258 2M0198H10	C 652	9.2	48.4	19	11	AZ761834	AZ761834 1M0556E19
580	9.4	49.5	24	11	BH789331	BH789331 SALK 0190	C 653	9.2	48.4	19	13	CL657666	CL657666 PR1012a.H
581	9.4	49.5	24	14	ATHS29294	ATHS29294 Arabidops	C 654	9.2	48.4	20	11	AZ388212	AZ388212 1M0148A10
582	9.4	49.5	25	1	AA894827	AA894827 oj61e08.s	C 655	9.2	48.4	21	9	DR063899	DR063899 ip71e12.g
583	9.4	49.5	25	1	AI174382	AI174382 an18f09.s	C 656	9.2	48.4	21	10	DV225120	DV225120 EST-AR103
584	9.4	49.5	25	1	AI364215	AI364215 qw38a07.x	C 657	9.2	48.4	21	10	DV225120	DV225120 EST-AR103
585	9.4	49.5	25	1	AI424019	AI424019 tf51e01.x	C 658	9.2	48.4	21	11	AZ321746	AZ321746 1M0042N20
586	9.4	49.5	25	1	AI445419	AI445419 tj34b12.x	C 659	9.2	48.4	21	11	AZ339828	AZ339828 1M0165A23
587	9.4	49.5	25	1	AI458062	AI458062 tj64c05.x	C 660	9.2	48.4	21	11	AZ632964	AZ632964 1M0487H22
588	9.4	49.5	25	1	AI565593	AI565593 tr93g08.x	C 661	9.2	48.4	22	1	AI582080	AI582080 ar96b07.x
589	9.4	49.5	25	1	AI632358	AI632358 to45a03.x	C 662	9.2	48.4	22	1	AI971767	AI971767 wv28a05.x
590	9.4	49.5	25	1	AI643068	AI643068 mo96g04.x	C 663	9.2	48.4	22	11	AZ640656	AZ640656 1M0502K14
591	9.4	49.5	25	1	AI762378	AI762378 w154f10.x	C 664	9.2	48.4	22	11	AZ958287	AZ958287 2M0225G02
592	9.4	49.5	25	1	AI808531	AI808531 wf95e12.x	C 665	9.2	48.4	23	2	BG924553	BG924553 HNC37-1-H
593	9.4	49.5	25	1	AI918365	AI918365 tr93c03.x	C 666	9.2	48.4	23	11	AZ499076	AZ499076 1M0336H08
594	9.4	49.5	25	1	AI971899	AI971899 wv29h04.x	C 667	9.2	48.4	23	11	AZ592207	AZ592207 1M0402N20
595	9.4	49.5	25	1	AJ802826	AJ802826 AJ802826	C 668	9.2	48.4	23	11	AZ595375	AZ595375 1M0407P19
596	9.4	49.5	25	5	CF313730	CF313730 HD--01-P1	C 669	9.2	48.4	23	11	AZ610186	AZ610186 1M0435R21
597	9.4	49.5	25	10	L32052	L32052 HUMXP464B.H	C 670	9.2	48.4	23	11	AZ774668	AZ774668 2M0004N08
598	9.4	49.5	25	11	AZ346741	AZ346741 1M0082C11	C 671	9.2	48.4	24	11	AZ600832	AZ600832 1M0418O14
599	9.4	49.5	25	11	AZ417946	AZ417946 1M0193O15	C 672	9.2	48.4	25	1	AI432500	AI432500 th35h06.x
600	9.4	49.5	25	11	AZ460726	AZ460726 1M0266O10	C 673	9.2	48.4	25	10	DW337978	DW337978 EST-AR042
601	9.4	49.5	25	11	AZ462642	AZ462642 1M0269M09	C 674	9.2	48.4	25	11	AZ441038	AZ441038 1M0232P20
602	9.4	49.5	25	11	AZ467031	AZ467031 1M0278H10	C 675	9.2	48.4	25	11	AZ468549	AZ468549 1M0281D10
603	9.4	49.5	26	11	AZ470860	AZ470860 1M0285K16	C 676	9.2	48.4	25	11	AZ620092	AZ620092 1M0452U07

C 677	9.2	48.4	25	11	AZ781710	AZ781710 2M0021E15	C 750	9	47.4	19	11	AZ427731	1M0209G1.9
C 678	9.2	48.4	25	11	BH146175	BH146175 EG02743-5	C 751	9	47.4	19	11	AZ427750	1M0209N1.9
C 679	9.2	48.4	25	13	CZ909373	CZ909373 4018009B0	C 752	9	47.4	19	11	AZ432920	1M0229B1.5
C 680	9.2	48.4	26	11	AZ768557	AZ768557 M0568B04	C 753	9	47.4	19	11	AZ446934	1M0243N01
C 681	9.2	48.4	26	11	AZ942099	AZ942099 2M0202C09	C 754	9	47.4	19	11	AZ447234	1M0244L16
C 682	9.2	48.4	26	14	AG188964	AG188964 Fan trogl	C 755	9	47.4	19	11	AZ447245	1M0244A22
C 683	9.2	48.4	27	11	AZ399752	AZ399752 1M0165D15	C 756	9	47.4	19	11	AZ466785	1M0277A16
C 684	9.2	48.4	27	11	AZ784820	AZ784820 2M0028N04	C 757	9	47.4	19	11	AZ468226	1M0281D10
C 685	9.2	48.4	27	11	AZ842796	AZ842796 2M0141120	C 758	9	47.4	19	11	AZ478905	1M0299E18
C 686	9.2	48.4	27	12	CG728385	CG728385 1119100A1	C 759	9	47.4	19	11	AZ481469	1M0303B15
C 687	9.2	48.4	28	1	AI434397	AI434397 t148R06.x	C 760	9	47.4	19	11	AZ493581	1M0328A24
C 688	9.2	48.4	28	1	AI444428	AI444428 fD38C12.x	C 761	9	47.4	19	11	AZ499200	1M0336O22
C 689	9.2	48.4	28	1	AI544609	AI544609 fB76E03.x	C 762	9	47.4	19	11	AZ579189	1M0363I12
C 690	9.2	48.4	28	1	A1686998	A1686998 tp81E01.x	C 763	9	47.4	19	11	AZ587841	1M0395J14
C 691	9.2	48.4	28	11	AZ584848	AZ584848 1M0389I13	C 764	9	47.4	19	11	AZ611179	1M0403B01
C 692	9.2	48.4	28	11	AZ594339	AZ594339 1M0406A21	C 765	9	47.4	19	11	AZ611509	1M0437E21
C 693	9.2	48.4	28	11	AZ594339	AZ594339 1M0406A21	C 766	9	47.4	19	11	AZ6115843	1M0445E23
C 694	9.2	48.4	28	13	CZ907925	CZ907925 4018001B0	C 767	9	47.4	19	11	AZ618258	1M0449G23
C 695	9.2	48.4	28	14	TAISO0BHP	AL057272 Drosophill	C 768	9	47.4	19	11	AZ625211	1M0464P22
C 696	9.2	48.4	28	14	CNS00B12P	AL464095 T. brucei	C 769	9	47.4	19	11	AZ625605	1M0465D17
C 697	9.2	48.4	29	1	AM043404	AM043404	C 770	9	47.4	19	11	AZ634205	1M0489D19
C 698	9.2	48.4	29	11	AZ406476	AZ406476 1M0175B15	C 771	9	47.4	19	11	AZ648703	1M0517A20
C 699	9.2	48.4	29	11	AZ438509	AZ438509 1M0228G08	C 772	9	47.4	19	11	AZ649856	1M0519O07
C 700	9.2	48.4	29	11	AZ774255	AZ774255 2M0003I24	C 773	9	47.4	19	11	AZ650212	1M0520G13
C 701	9.2	48.4	29	11	AZ783480	AZ783480 2M0025F14	C 774	9	47.4	19	11	AZ654733	1M0529A09
C 702	9.2	48.4	29	11	AZ805819	AZ805819 2M0067K19	C 775	9	47.4	19	11	AZ654842	1M0529A30
C 703	9.2	48.4	29	11	AZ805819	AZ805819 2M0067K19	C 776	9	47.4	19	11	AZ656937	1M0532K13
C 704	9.2	48.4	29	11	AZ854411	AZ854411 2M0158B05	C 777	9	47.4	19	11	AZ657564	1M0533P18
C 705	9.2	48.4	29	11	BH856361	BH856361 SALK_0798	C 778	9	47.4	19	11	AZ764495	1M0560G06
C 706	9.2	48.4	29	12	BZ595262	BZ595262 SALK_0863	C 779	9	47.4	19	11	AZ764500	1M0560K06
C 707	9.2	48.4	29	13	CZ908389	CZ908389 4018002H0	C 780	9	47.4	19	11	AZ764526	1M0569K05
C 708	9.2	48.4	29	13	CL653182	CL653182 PRI0116d	C 781	9	47.4	19	11	AZ769239	1M0569K09
C 709	9.2	48.4	30	7	BE295129	BE295129 601173573	C 782	9	47.4	19	11	AZ783420	2M0025D07
C 710	9.2	48.4	30	11	AZ456295	AZ456295 1M0259J04	C 783	9	47.4	19	11	AZ786434	2M0031M24
C 711	9.2	48.4	30	11	AZ801555	AZ801555 2M0060M01	C 784	9	47.4	19	11	AZ795057	2M0049B08
C 712	9.2	48.4	30	11	AZ804486	AZ804486 2M0065D07	C 785	9	47.4	19	11	AZ798934	2M0056F01
C 713	9.2	48.4	30	13	CZ476117	CZ476117 d08201-3p	C 786	9	47.4	19	11	AZ799886	2M0057C12
C 714	9.2	48.4	30	13	CZ909411	CZ909411 4018009C0	C 787	9	47.4	19	11	AZ802234	2M0060M21
C 715	9.2	48.4	30	14	AB082245	AB082245 Drosophill	C 788	9	47.4	19	11	AZ808113	2M0071A01
C 716	9.2	48.4	30	14	CR359171	CR359171 Arabidops	C 789	9	47.4	19	11	AZ820788	2M0093A16
C 717	9	47.4	11	1	AJ648107	AJ648107 Arabidops	C 790	9	47.4	19	11	AZ843215	2M0142B06
C 718	9	47.4	17	9	DN986658	DN986658 MSU_28R_2	C 791	9	47.4	19	11	AZ845178	2M0144P16
C 719	9	47.4	17	14	AJ599163	AJ599163 Arabidops	C 792	9	47.4	19	11	AZ849133	2M0150L21
C 720	9	47.4	19	1	AA911671	AA911671 Ol49f08.s	C 793	9	47.4	19	11	AZ854647	2M0158P15
C 721	9	47.4	19	1	AI142547	AI142547 QB47D08.x	C 794	9	47.4	19	11	AZ854647	2M0158P15
C 722	9	47.4	19	1	AI471695	AI471695 t199F04.x	C 795	9	47.4	19	11	AZ861541	2M0168F19
C 723	9	47.4	19	1	AI683556	AI683556 tx67R08.x	C 796	9	47.4	19	11	AZ941561	2M0201B19
C 724	9	47.4	19	1	AI718147	AI718147 ab42F11.x	C 797	9	47.4	19	11	AZ969354	2M0242A07
C 725	9	47.4	19	1	AJ7659543	AJ7659543 AJ659543	C 798	9	47.4	19	13	CL665369	2M0242A07
C 726	9	47.4	19	1	AJ747090	AJ747090 AJ747090	C 799	9	47.4	20	5	CF279207	FR10149C-
C 727	9	47.4	19	1	AM075425	AM075425 AM075425	C 800	9	47.4	20	5	CF302797	14ETL--05
C 728	9	47.4	19	1	CA794263	CA794263 Cdc_B1_12	C 801	9	47.4	20	5	CF302797	7LEAF--08
C 729	9	47.4	19	5	CF280692	CF280692 14ETL--07	C 802	9	47.4	20	5	CF309954	ABF--04-F
C 730	9	47.4	19	5	CF282249	CF282249 14ETL--09	C 803	9	47.4	20	5	CF311285	ABF--06-H
C 731	9	47.4	19	5	CF295184	CF295184 30DGS--05	C 804	9	47.4	20	5	CF312611	ABF--08-H
C 732	9	47.4	19	5	CF312583	CF312583 ABF--08-G	C 805	9	47.4	20	5	CF313735	HD--07-A1
C 733	9	47.4	19	5	CF323353	CF323353 HDN--03-K	C 806	9	47.4	20	5	CF317375	JMT--07-O
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ALIGNMENTS

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              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 28)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
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ORIGIN

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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 4 GGAGAGGGGGTGGGTG 20

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DEFINITION clone UUGClM0010L24 F, genomic survey sequence.
ACCESSION AZ307952
VERSION AZ307952.1 GI:10347459
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
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ORIGIN
Query Match 70.5%; Score 13.4; DB 11; Length 22;
Best Local Similarity 93.3%; Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGAGAGGGGGTGGG 15
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Db 4 GGAGAGGGGGTGGG 18

RESULT 3
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LOCUS
DEFINITION
to73c10.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2183922 3,
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ACCESSION
A1673793
VERSION
A1673793.1 GI:4853524
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1546 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
source
1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2183922"
/tissue_type="poorly differentiated adenocarcinoma with signed ring cell features"
/lab host="DH10B"
/clone lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 Kb. Life Technologies catalog #: 11549-011"

ORIGIN
Query Match 69.5%; Score 13.2; DB 1; Length 22;
Best Local Similarity 83.3%; Pred. No. 4.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTGCT 19
|||||
Db 1 GAGAGGGGGGGGTGTT 18

RESULT 4
A1586975
LOCUS
DEFINITION
tw15q05.x1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2259800 3,
similar to SW:EXTN_TOBAC F13983 EXTENSIN PRECURSOR ;, mRNA
sequence.
ACCESSION
A1586975
VERSION
A1586975.1 GI:4573416
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 25)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
source
1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2259800"
/tissue_type="tumor, 5 pooled (see description)"
/lab host="DH10B"
/clone lib="NCI CGAP Brn52"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; This library represents the normalized version of NCI CGAP Brn52. Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.19 kb. Tumor types include: meningioma, oligodendroglioma, astrocytoma (grade II), medulloblastoma, astrocytoma (grade IV). Constructed by Life Technologies."

ORIGIN
Query Match 67.4%; Score 12.8; DB 1; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGGTG 17
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Db 3 GGGGAAGGGGGGGG 19

RESULT 5
BQ590098
LOCUS
DEFINITION
E012843-024-019-019-T7 MP12-ADIS-024-storage root Beta vulgaris
ACCESSION
BQ590098
VERSION
BQ590098.1 GI:26119681
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 29)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radeflof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
PUBMED
12472698
COMMENT
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 19 row: O column: 19
Seq primer: T7; GTAATACGACTCATATAGGC.
FEATURES
source
1..29
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:190019"
/db_xref="taxon:161934"
/clone="024-019-019"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: PCWVSORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 67.4%; Score 12.8; DB 3; Length 29;
Best Local Similarity 87.5%; Pred. No. 6.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAAAGGGGGGGGGT 17
|||||
Db 13 GAGAAAGGGGGGGGGG 28

RESULT 6
A2479594
LOCUS
DEFINITION
IM0300822F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0300822 F, genomic survey sequence.
ACCESSION
A2479594
VERSION
A2479594.1 GI:10639102

KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0300 row: B column: 22
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES
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1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0300B22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 66.3%; Score 12.6; DB 11; Length 22;
Best Local Similarity 78.9%; Pred. No. 7.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGGGTGTCT 19
|||||
Db 3 GGGTAATGTGTGTGTGTCT 21

RESULT 7
A2345548/c
LOCUS
DEFINITION
1M0080D13F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0080D13 F, genomic survey sequence.
ACCESSION
A2345548

```

VERSION AZ486450.1 GI:10424785
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: D column: 13
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080D13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 65.3%; Score 12.4; DB 11; Length 20;
Best Local Similarity 92.9%; Pred. No. 9.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGAGGGGGGTGGG 15
|||||
DB 19 GAGAGGGGGGTGGG 6

RESULT 8
AZ486450 24 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0314A06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0314A06 R, genomic survey sequence.

```

```

ACCESSION AZ486450
VERSION AZ486450.1 GI:10653235
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0314 row: A column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0314A06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 65.3%; Score 12.4; DB 11; Length 24;
Best Local Similarity 92.9%; Pred. No. 9.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGAGGGGGGTGGG 15
|||||
DB 4 GAGAGGGGGGTGGG 17

RESULT 9
AI000026 22 bp mRNA linear EST 05-JUN-1998
LOCUS AI000026
DEFINITION ot03d12.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613783 3'

```

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AI000026 AI000026.1 GI:3190580 EST. Homo sapiens (human)	similar to TR:Q92853 Q92853 HU-K4. ;, mRNA sequence.
REFERENCE AUTHORS TITLE JOURNAL COMMENT	1 (bases 1 to 22) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: c9apbs-r@mail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html	
FEATURES source	Trace considered overall poor quality Seq primer: -40m13 fwd. Et from Amersham High quality sequence stop: 1. Location/Qualifiers 1..22 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1613783" /tissue_type="pooled germ cell tumors" /lab_host="DH10B" /clone_lib="NCI CGAP GC3" /note="Vector: pTT3D-PacI; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."	
ORIGIN	Query Match 64.2%; Score 12.2; DB 1; Length 22; Best Local Similarity 82.4%; Pred. No. 1.1e+06; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0; QY 1 CGAGAGGGGGTGGGTG 17 DB 6 GCACAAAGGGGTGGGGG 22	
RESULT 10 AZ792883 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AZ792883 2M0045J09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0045J09 R, genomic survey sequence. AZ792883 AZ792883.1 GI:12937268 GSS. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus. 1 (bases 1 to 22) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	
REFERENCE AUTHORS		
TITLE JOURNAL COMMENT	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0045 row: J column: 09 Seq primer: CACACAGGACACAGCTATGACC Class: plasmid ends High quality sequence stop: 22. Location/Qualifiers 1..22 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0045J09" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
ORIGIN	Query Match 64.2%; Score 12.2; DB 1; Length 22; Best Local Similarity 82.4%; Pred. No. 1.1e+06; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0; QY 1 CGAGAGGGGGTGGGTG 17 DB 2 GTAGAGTGGGTGGGTG 18	
RESULT 11 AZ800080 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AZ800080 2M0057122R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0057122 R, genomic survey sequence. AZ800080 AZ800080.1 GI:12951848 GSS. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 23) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von	
REFERENCE AUTHORS		

TITLE Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0057 row: I column: 22
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.

FEATURES
source

1. 23
/location="Guarillais"
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0057122"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1/4732114[gbl]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match	64.2%	Score 12.2;	DB 11;	Length 23;
Best Local Similarity	82.4%;	Pred. No. 1.1e+06;		
Matches 14;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	3	AGAAAGGGGGTGGTGCT	19	
Db	1	AGGAGGGGGTTGGAGCT	17	

RESULT 12	AZ943422/c
LOCUS	25 bp DNA linear GSS 26-APR-2001
DEFINITION	2M0204P06F Mouse 10kb plasmid UGCG2M library Mus musculus genomic clone UGCG2M0204P06 F, genomic survey sequence.
ACCESSION	AZ943422
VERSION	AZ943422.1 GI:13807481
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 25)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0204 row: P column: 06
Seq primer: CCGTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 25.

FEATURES
source

ORIGIN

Query Match	64.2%	Score 12.2;	DB 11;	Length 25;
Best Local Similarity	82.4%;	Pred. No. 1.1e+06;		
Matches 14;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	GGAGGAAGGGGTGGGTG	17	
Db	23	GGCGAAGGGGGGGGGG	7	

RESULT	13
LOCUS	AZ362697
DEFINITION	AZ362697 Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0107623 R, genomic survey sequence.
ACCESSION	AZ362697
VERSION	AZ362697.1 GI:10476397
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 26)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

REFERENCES

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: G column: 23
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0107G23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTG 17

Db 8 GGGGGTGGGGGGTGGGTG 24

RESULT 14

AZ836891

LOCUS

2M0131N22R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0131N22 R, genomic survey sequence.

DEFINITION

AZ836891

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

(house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 27)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0131 row: N column: 22
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0131N22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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inducible derivative of plasmid R1. The vector was ligated
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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTG 17

Db 11 GGAGACGGGGGGGGGGG 27

RESULT 15

AI785472/c

LOCUS

uJ42f07 xl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1922629 3' similar to SW:RLX1_HUMAN P49406 PUTATIVE 60S
RIBOSOMAL PROTEIN. ;, mRNA sequence.

DEFINITION

AI785472

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

(house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE
AUTHORS

Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 28)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterson, R., and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Other ESTs: u342f07.y1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:978921

TITLE
JOURNAL
COMMENT

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1922629"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACCCTGTG); Site_2: DraIII (CACCCTGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [GTGGCGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCCTGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGGG and 3' end
primer CGACTGCGAGCTCGACACA."

FEATURES
source

ORIGIN

Query Match 64.2%; Score 12.2; DB 1; Length 28;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGGGTG 17
|||||
Db 23 GGAGAAGGGGTGGATG 7

RESULT 16
AZ483923/c
LOCUS
DEFINITION
1M0309A22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0309A22 R, genomic survey sequence.

ACCESSION
AZ483923
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 28)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0309 row: A column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0309A22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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inducible derivative of plasmid R1. The vector was ligated
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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 28;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGGGTG 17
|||||
Db 21 GGGAAGGGGGGGGGG 5

RESULT 17
AZ2774078/c
LOCUS
DEFINITION
2M0003001F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0003001 F, genomic survey sequence.

ACCESSION
AZ2774078
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 28)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0106 row: E column: 01
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.

FEATURES
source

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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0106E01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 30;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAGAGAGGGGGTGGGGT 17
DB 3 GAAGCAGAGGGGGTGGGGG 19

RESULT 20
AZ405596
LOCUS
DEFINITION
1M0174B06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0174B06 R, genomic survey sequence.
ACCESSION
AZ405596
VERSION
AZ405596.1 GI:10529609
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0174 row: B column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source

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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0174B06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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inducible derivative of plasmid R1. The vector was ligated
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purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGAGAGAGGGGGTGGG 15
DB 2 GGGGAGAGGGGGTGGG 16

RESULT 21
AZ445481/c
LOCUS
DEFINITION
1M0241P15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0241P15 F, genomic survey sequence.
ACCESSION
AZ445481
VERSION
AZ445481.1 GI:10595346
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0241 row: P column: 15
Seq primer: CTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0241P15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 21;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGGTGGG 15
||| |||||
Db 17 GCATATGGGGTGGG 3

RESULT 22
AZ816100/c
LOCUS AZ816100 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0084M11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0084M11 R, genomic survey sequence.
ACCESSION AZ816100
VERSION AZ816100.1 GI:12986008
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

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AUTHORS 1 (bases 1 to 21)
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

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COMMENT Unpublished (2000)
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0084 row: M column: 11
Seq primer: CACACAGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source
1..21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0084M11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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10.5 kb range using preparative agarose gel
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ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 21;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAGGGGTGGGTGCT 19
||| |||||
Db 21 AAGTGGGTGGGGCT 7

RESULT 23
AZ834089/c
LOCUS AZ834089 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0116C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0116C12 R, genomic survey sequence.
ACCESSION AZ834089
VERSION AZ834089.1 GI:13003997
KEYWORDS GSS.

SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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JOURNAL
Contact: Robert B. Weiss
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University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0116 row: C column: 12
Seq primer: CACACGAGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0116C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 62.1%; Score 11.8; DB 11; Length 21;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGAGAAAGGGGGTGGG 15
||| ||||| |||||
Db 16 GGGGAAGGGGGGGGG 2

RESULT 24
BH000494
LOCUS BH000494 24 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0288H21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0288H21 F, genomic survey sequence.
ACCESSION BH000494
VERSION BH000494.1 GI:13871720

KEYWORDS
GSS.
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
Contact: Robert B. Weiss
COMMENT
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: H column: 21
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288H21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 62.1%; Score 11.8; DB 11; Length 24;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGAGAAAGGGGGTGGG 15
||| ||||| |||||
Db 10 GGAGAGGGGGGGGGG 24

RESULT 25
AA878831
LOCUS AA878831 25 bp mRNA linear EST 25-MAR-1998
DEFINITION of83f10.81 NCI CGAP L15 Homo sapiens cDNA clone IMAGE:1436971 3'
similar to TR:Q43687 Q43687 EXTENSIN-LIKE PROTEIN ;contains MSRI.b1
TARI repetitive element ;, mRNA sequence.

```

ACCESSION      AA878831
VERSION        AA878831.1  GI:2987796
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1 (bases 1 to 25)
               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
               Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               unknown library type
               Trace considered overall poor quality
               Seq primer: -40m13 fwd. ET from Amersham
               High quality sequence stop: 1.
FEATURES       Location/Qualifiers
               1..25
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:1436971"
               /tissue_type="hepatic adenoma"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP L15"
               /note="Organ: liver; Vector: pCMV-SPORT4; Site: 1: Salt;
               Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 0.8 kb."
ORIGIN
Query Match      62.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGAGAGGGGGGTGGG 15
    |||||
Db 3 CGAGGGGGGGGTGGG 17

RESULT 26
LOCUS      AI628239
DEFINITION ty93c04.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:2286630 3'
            similar to TR:Q01944 Q01944 EXTENSIN ;contains element MSR1
            repetitive element ;, mRNA sequence.
ACCESSION  AI628239
VERSION     AI628239.1  GI:4665039
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 25)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Trace considered overall poor quality

ACCESSION      AA878831
VERSION        AA878831.1  GI:2987796
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1 (bases 1 to 25)
               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
               Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               unknown library type
               Trace considered overall poor quality
               Seq primer: -40m13 fwd. ET from Amersham
               High quality sequence stop: 1.
FEATURES       Location/Qualifiers
               1..25
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:1436971"
               /tissue_type="hepatic adenoma"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP L15"
               /note="Organ: liver; Vector: pCMV-SPORT4; Site: 1: Salt;
               Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 0.8 kb."
ORIGIN
Query Match      62.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGAGAGGGGGGTGGG 15
    |||||
Db 3 CGAGGGGGGGGTGGG 17

RESULT 26
LOCUS      AI628239
DEFINITION ty93c04.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:2286630 3'
            similar to TR:Q01944 Q01944 EXTENSIN ;contains element MSR1
            repetitive element ;, mRNA sequence.
ACCESSION  AI628239
VERSION     AI628239.1  GI:4665039
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 25)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Trace considered overall poor quality

Insert Length: 1021 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
FEATURES       Location/Qualifiers
               1..25
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:2286630"
               /tissue_type="well-differentiated endometrial
               adenocarcinoma, 7 pooled tumors"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP Utl"
               /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
               Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 1.75 Kb. Life Technologies catalog #:
               11538-014"
ORIGIN
Query Match      62.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGGTGGGTG 17
    |||||
Db 1 AGAAGGGGGGGGGGG 15

RESULT 27
LOCUS      AZ391369
DEFINITION clone UUGC1M0153K24 F, genomic survey sequence.
ACCESSION  AZ391369
VERSION     AZ391369.1  GI:10506412
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
            1 (bases 1 to 25)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
            Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES       Location/Qualifiers
               1..25
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0153K24"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"

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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGG 15
|||||
Db 8 GGAGAGGGGGGGGG 22

RESULT 28

AZ772979

LOCUS

DEFINITION 1M0584E13F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0584E13 F, genomic survey sequence.

ACCESSION

AZ772979

VERSION

GSS.

SOURCE

Mus musculus

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0584 row: E column: 13

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1..25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUC1M0584E13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTG 17
|||||
Db 3 AAAGGGAGTGGGTG 17

RESULT 29

AZ843200

LOCUS

DEFINITION 2M0141024R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC2M0141024 R, genomic survey sequence.

ACCESSION

AZ843200

VERSION

GSS.

KEYWORDS

SOURCE

Mus musculus

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0141 row: O column: 24

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

1..26

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUC2M0141024"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 26;
 Best Local Similarity 86.7%; Pred. No. 1.6e+06;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGGTG 17
 | | | | | | | | | |
 Db 1 AAAAGGAGTGGGTG 15

RESULT 30

AZ477874/c
 LOCUS
 DEFINITION 28 bp DNA linear GSS 04-OCT-2000
 clone UUGC1M0297022 F, genomic survey sequence.

ACCESSION AZ477874
 VERSION AZ477874.1 GI:10636044
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0297 row: 0 column: 22

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1..28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0297022"

FEATURES

source

1..28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/sex="Male"
 /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 28;
 Best Local Similarity 86.7%; Pred. No. 1.6e+06;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGGTG 17
 | | | | | | | | | |
 Db 19 ATAAGGGGTGGGTG 5

RESULT 31

AZ489682
 LOCUS
 DEFINITION 28 bp DNA linear GSS 05-OCT-2000
 clone UUGC1M0322G16 F, genomic survey sequence.

ACCESSION AZ489682
 VERSION AZ489682.1 GI:10659670
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0322 row: G column: 16

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1..28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

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/clone="UUGC1M0322G16"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/sex="Male"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 62.1%; Score 11.8; DB 11; Length 28;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGGTG 17
Db ||||| ||||| |||||
7 AGAAGTGGGGGGGTG 21

RESULT 32
LOCUS CX012159 29 bp mRNA linear EST 06-DEC-2004
DEFINITION io57g07.b1 Whole Heart Library (DOGEST5) Canis familiaris cDNA, mRNA sequence.
ACCESSION CX012159.1 GI:56394570
VERSION CX012159.1
KEYWORDS EST:
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 29)
AUTHORS Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris whole heart (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Auenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Location/Qualifiers
1..29
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGEST5)"
/note="Organ: Heart; Vector: pBluescript II SK; Site: 1: EcoRI; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street,

/clone="UUGC1M0322G16"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/sex="Male"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 62.1%; Score 11.8; DB 8; Length 29;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTG 16
Db ||||| ||||| |||||
11 GTGCAGGGGGTGGGTG 25

RESULT 33
LOCUS AI758492 22 bp mRNA linear EST 16-DEC-1999
DEFINITION ty08d06.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2278475 3', similar to TR:048803 U48809 F24O1.18.;, mRNA sequence.
ACCESSION AI758492
VERSION AI758492.1 GI:5152215
KEYWORDS EST:
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 22)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 736 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2278475"
/tissue_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI-CGAP Ut3"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"

ORIGIN
Query Match 61.1%; Score 11.6; DB 1; Length 22;
Best Local Similarity 77.8%; Pred. No. 2e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGGTGC 18
Db ||||| ||||| |||||
21 GCGCAGGGGGGGGGGGC 4

RESULT 34
LOCUS AZ627855 24 bp DNA linear GSS 13-DEC-2000

```

DEFINITION 1M0476C06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0476C06 F, genomic survey sequence.

ACCESSION AZ627855

VERSION AZ627855.1 GI:11750141

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: C column: 06
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source
1..24
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0476C06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 61.1%; Score 11.6; DB 11; Length 24;
Best Local Similarity 77.8%; Pred. No. 2e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGAGAAGGGGGTGGGTGC 18
||| ||||| ||||| |||

Db 3 GGGAAAAGGGGTGGGTTC 20

RESULT 35
CZ915711/c

LOCUS CZ915711 27 bp DNA linear GSS 08-AUG-2005

DEFINITION 4013012GI2.2EL_xl 4013 - RescueMu Grid O Zea mays genomic survey sequence.

ACCESSION CZ915711

VERSION CZ915711.1 GI:71933250

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 27)

Walbot,V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013012 row: G column: 12
Class: transposon-tagged.

FEATURES

source
1..27
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/culturivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 61.1%; Score 11.6; DB 13; Length 27;
Best Local Similarity 77.8%; Pred. No. 2e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGAGAAGGGGGTGGGTGC 18
||| ||||| ||||| |||

Db 18 GGGGAGGGGGGGGGGGGC 1

RESULT 36
BM396069

LOCUS BM396069 29 bp mRNA linear EST 17-JAN-2002

DEFINITION 5009-0-16-F06.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM396069

VERSION BM396069.1 GI:18196122

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena. 1 (bases 1 to 29)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,

TITLE EST from *Tetrahymena thermophila*, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1..29
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="vector: Bluescript2 SK+; details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

```

ORIGIN
      110:      120:      130:      140:      150:      160:      170:      180:      190:      200:
Query Match          61.1%; Score 11.6; DB 2; Length 29;
Best Local Similarity 77.8%; Pred. No. 2e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGAGAGGGGGTGGGTGC 18
      |||||
      |||||
Db 6 GGAGCTCCGGTGGGTGC 23
      |||||
      |||||

```

RESULT	37
AZ853274/c	
LOCUS	
DEFINITION	linear GSS 21-FEB-2001 Mmusculus genomic clone UGUC2M0156D23 F, genomic survey sequence.
ACCESSION	AZ853274
VERSION	AZ853274.1 GI:13041223
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 30) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.Weiss.R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., UT 84112, USA	
TITLE	
JOURNAL	
COMMENT	

```

Email: quinn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0156 row: D column: 23
Seq primer: CGTTTAAACACGCGGCAGT
Class: plasmid ends
High quality sequence stop: 30.
      Location/Qualifiers
          1..30
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UTGCG2M0156D23"

```

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/vector="PMD2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```

Query Match          61.1%; Score 11.6; DB 11; Length 30;
Best Local Similarity 77.8%; Pred. No. 2a+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY . 1 GGAGAGGGGGTGGTGC 18
Db 18 GGGGAGGGGGGGGGGC 1

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RESULT 38	13 bp	linear	EST 06-NOV-2001
LOCUS	13 bp	mRNA	EST 06-NOV-2001
DEFINITION	13 bp	mRNA	EST 06-NOV-2001
ACCESSION	13 bp	mRNA	EST 06-NOV-2001
VERSION	13 bp	mRNA	EST 06-NOV-2001
KEYWORDS	13 bp	mRNA	EST 06-NOV-2001
SOURCE	13 bp	mRNA	EST 06-NOV-2001
ORGANISM	13 bp	mRNA	EST 06-NOV-2001
REFERENCE	13 bp	mRNA	EST 06-NOV-2001
AUTHORS	13 bp	mRNA	EST 06-NOV-2001
TITLE	13 bp	mRNA	EST 06-NOV-2001
JOURNAL	13 bp	mRNA	EST 06-NOV-2001
PUBLISHED	13 bp	mRNA	EST 06-NOV-2001

FEATURES	SOURCE
1. Geographical Location: The study area is located in the northern part of the state, covering a total area of 100 square kilometers.	1. Geographical Location: The study area is located in the northern part of the state, covering a total area of 100 square kilometers.
2. Population: The population of the study area is approximately 50,000 people, with a significant portion being rural.	2. Population: The population of the study area is approximately 50,000 people, with a significant portion being rural.
3. Climate: The climate is semi-arid, with hot summers and mild winters. The average annual rainfall is 1,200 mm.	3. Climate: The climate is semi-arid, with hot summers and mild winters. The average annual rainfall is 1,200 mm.
4. Topography: The topography is mostly flat, with some low hills and valleys.	4. Topography: The topography is mostly flat, with some low hills and valleys.
5. Vegetation: The vegetation is primarily dry forest and scrubland.	5. Vegetation: The vegetation is primarily dry forest and scrubland.
6. Soil: The soil is mostly sandy and loamy, with some clayey areas.	6. Soil: The soil is mostly sandy and loamy, with some clayey areas.
7. Water Resources: The study area has several rivers and streams, but the water quality is poor due to pollution.	7. Water Resources: The study area has several rivers and streams, but the water quality is poor due to pollution.
8. Infrastructure: The infrastructure is basic, with a few roads and a small airport.	8. Infrastructure: The infrastructure is basic, with a few roads and a small airport.
9. Economy: The economy is primarily based on agriculture and tourism.	9. Economy: The economy is primarily based on agriculture and tourism.
10. Education: The education level is low, with only a few schools and colleges.	10. Education: The education level is low, with only a few schools and colleges.
11. Healthcare: The healthcare system is underdeveloped, with only a few clinics and hospitals.	11. Healthcare: The healthcare system is underdeveloped, with only a few clinics and hospitals.
12. Environment: The environment is facing several challenges, including deforestation and air pollution.	12. Environment: The environment is facing several challenges, including deforestation and air pollution.

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
directional"

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ORIGIN		and selected for ampicillin resistance."	
Query Match	60.0%;	Score 11.4;	DB 2; Length 13;
Best Local Similarity	92.3%;	Pred. No. 2.4e+06;	
Matches	12; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
QY	1	GGAGAAGGGGGTG 13	
Db	13	GGAGAAGGGGGAG 1	
RESULT 39			
AZ787717			
LOCUS	AZ787717 19 bp DNA linear GSS 16-FEB-2001		
DEFINITION	2M0034A21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0034A21 F, genomic survey sequence.		
ACCESSION	AZ787717		
VERSION	AZ787717.1 GI:12926787		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0034 row: A column: 21 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 19.		
FEATURES		source	
1..19		Location/Qualifiers	
		/organism="Mus musculus"	
		/mol_type="genomic DNA"	
		/strain="C57BL/6J"	
		/db_xref="taxon:10090"	
		/clone="UUGC2M0034A21"	
		/sex="Male"	
		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	
		/clone_lib="Mouse 10kb plasmid UUGC1M library"	
		/note="Vector: PWD42v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells	

ORIGIN		and selected for ampicillin resistance."	
Query Match	60.0%;	Score 11.4;	DB 11; Length 19;
Best Local Similarity	92.3%;	Pred. No. 2.4e+06;	
Matches	12; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
QY	7	GGGGGTGGGTGCT 19	
Db	1	GGGGGTGGGTACT 13	
RESULT 40			
AI439277/c			
LOCUS	AI439277 22 bp mRNA linear EST 09-MAR-1999		
DEFINITION	tis4a02.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134250 3', similar to TR.Q17089 Q17089 COLLAGEN ;contains element MER22 repetitive element ;, mRNA sequence.		
ACCESSION	AI439277		
VERSION	AI439277.1 GI:4303196		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 22)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Life Technologies catalog #: 11547-015 DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html		
Trace considered overall poor quality		Seq primer: -40UP from Gibco	
High quality sequence stop: 1.		Location/Qualifiers	
1..22		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:2134250"	
		/tissue_type="lymphoma, follicular mixed small and large cell"	
		/lab_host="DH10B"	
		/clone_lib="NCI_CGAP Lym12"	
		/note="Organ: lymph node; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"	

ORIGIN		Query Match 60.0%; Score 11.4; DB 1; Length 22;	
Best Local Similarity 92.3%; Pred. No. 2.4e+06;		Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	5	AAGGGGGTGGGTG 17	
Db	21	AAGGGGGGGGGTG 9	
RESULT 41			
AZ351959			
LOCUS	AZ351959 22 bp DNA linear GSS 29-SEP-2000		
DEFINITION	1M0090C16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0090C16 F, genomic survey sequence.		
ACCESSION	AZ351959		

```

VERSION AZ351959.1 GI:10431196
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0090 row: C column: 16
Seq primer: CCGTGTAAACACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0090C16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0172119"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 60.0%; Score 11.4; DB 11; Length 22;
Best Local Similarity 92.3%; Pred. No. 2.4e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAGGGGGTGGGTG 17
DB 6 ATGGGGGTGGGTG 18

RESULT 42
AZ404383 23 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0172119R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0172119 R, genomic survey sequence.

ACCESSION AZ404383
VERSION AZ404383.1 GI:10528492
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: I column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0172119"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 60.0%; Score 11.4; DB 11; Length 23;
Best Local Similarity 92.3%; Pred. No. 2.4e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGGGGTGGGTGCT 19
DB 1 GGGGGTGGGTGCT 13

RESULT 43
AI066777/C 25 bp mRNA linear EST 31-JUL-1998
LOCUS AI066777
DEFINITION ov17a05.x1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1637552 3'

```

similar to TR:Q39599 Q39599 EXTENSIN. ; contains MSR1.t2 MSRI
repetitive element ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AI066777.1 GI:3367063
EST.

Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

1 (bases 1 to 25)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40m13 fwd. Et from AmerSham

High quality sequence stop: 1.

FEATURES
source

1..25

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1637552"

/tissue_type="pooled germ cell tumors"

/lab_host="DH10B"

/clone_lib="NCI CGAP GC3"

/note="Vector: pRTT3D-PacI; 1st strand cDNA was prepared
from 3 pooled germ cell tumors, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pRTT3 vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 60.0%; Score 11.4; DB 1; Length 25;
Best Local Similarity 92.3%; Pred. No. 2.4e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGG 15

Db 13 AAAAGGGGGTGGG 1

RESULT 44
LOCUS

DU777397
DEFINITION
ASXB1637.b2 HF500_10-06-02 uncultured marine microorganism
HF500_10-06-02 genomic clone HF0500_077E01, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DU777397.1 GI:85791593

GSS.

uncultured marine microorganism HF500_10-06-02

uncultured marine microorganism HF500_10-06-02

unclassified sequences; environmental samples.

1 (bases 1 to 27)

DeLong,E.F., Presnott,C.M., Mincer,T., Rich,V., Hallam,S.J.,
Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.
and Karl,D.M.

Comparative genomics reveals ecological trends in stratified

JOURNAL
COMMENT

microbial communities in the ocean's interior
Science (2006) In press
Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
Kerrie Barry, Rijana Glavinadelrio, David Bruce, Paul Richardson
and Edward DeLong
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-2679
Email: PMRichardson@lbl.gov; delong@mit.edu

North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6
um, greater than 0.22 um fraction. Sample Date: 10/6/2002
Coordinates: 22.45 N, 158 W Depth 500 m Temperature: 7.25 C
Salinity: 34.07 psu Oxygen: 118.0 umol/kg
Class: fosmid ends.

FEATURES
source

1..27

/organism="uncultured marine microorganism HF500_10-06-02"

/mol_type="genomic DNA"

/db_xref="taxon:361149"

/clones="HF0500_077E01"

/cell_type="marine picoplankton, less than 1.8 um, greater
than 0.22 um fraction"

/clone_lib="HF500_10-06-02"

/note="Vector: pCC1FOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 500 m
depth on 10/6/2002, Coordinates: 22.45 N, 158 W. Sample
Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 500 m
Temperature: 7.25 C Salinity: 34.07 psu Oxygen: 118.0
umol/kg"

ORIGIN

Query Match 60.0%; Score 11.4; DB 14; Length 27;

Best Local Similarity 85.7%; Pred. No. 2.4e+06;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGG 14

Db 13 GGAGAGGGGGGGG 26

RESULT 45
AI567156/c

LOCUS

DEFINITION

AI567156 28 bp mRNA linear EST 13-MAY-1999

tp50b06.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2191187 3'

similar to TR:Q39600 Q39600 EXTENSIN. ;, mRNA sequence.

ACCESSION

AI567156

VERSION

AI567156.1 GI:4525608

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo

1 (bases 1 to 28)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality
 Insert length: 2563 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1
 POLYA=No.

FEATURES

source

Location/Qualifiers

1. .28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2191187"
 /tissue_type="serous papillary carcinoma, high grade, 2
 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Ut4"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.48 Kb. Life technologies catalog #: 11542-016"

ORIGIN

Query Match 60.0%; Score 11.4; DB 1; Length 28;
 Best Local Similarity 92.3%; Pred. No. 2.4e+06;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 GGAGAAGGGGGTG 13

|||||

Db

15 GGGGAAGGGGGTG 3

RESULT 46

DN988622

LOCUS

DN988622 20 bp mRNA linear EST 17-MAY-2005
 ZEBRA_28R_2-II_02_ZEBRA_28R_2-II_02_E09.ab1 Bermudagrass line Zebra
 subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone

ZEBRA_28R_2-II_02_ZEBRA_28R_2-II_02_E09.ab1, mRNA sequence.

DN988622

DN988622.1 GI:66248449

EST.

Cynodon dactylon (Bermuda grass)

Cynodon dactylon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Chloridoideae; Cynodonteae; Cynodon.

1 (bases 1 to 20)

Melmaiee, K., Elavarthi, S. and Guenzi, A.C.

Identification of differentially expressed genes associated with
 cold acclimation using suppression subtraction hybridization (SSH)

and cDNA microarrays

Unpublished (2005)

Contact: Guenzi AC

Dep. of Plant and Soil Sciences

Oklahoma State University

368 Agriculture Hall, Stillwater, OK 74078-6028, USA

Tel: 405-744-6028

Fax: 405-744-6039

Email: acg@mail.pss.okstate.edu

PCR Primers

FORWARD: M13 forward

BACKWARD: M13 Reverse

Seq primer: M13 Forward.

FEATURES

source

Location/Qualifiers

1. .20
 /organism="Cynodon dactylon"
 /mol_type="mRNA"
 /cultivar="Zebra"
 /db_xref="taxon:28909"
 /clone="ZEBRA_28R_2-II_02_ZEBRA_28R_2-II_02_E09.ab1"
 /tissue_type="crown"
 /lab_host="E. coli"
 /clone_lib="Bermudagrass line Zebra subtracted cold
 acclimated cDNA library"

ORIGIN

Query Match 58.9%; Score 11.2; DB 9; Length 20;
 Best Local Similarity 81.2%; Pred. No. 2.9e+06;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

3 AGAAGGGGGTGGTGC 18

Db

5 AAAAGGGGGGGGAGC 20

RESULT 47

AZ864022

LOCUS

AZ864022 21 bp DNA linear GSS 21-FEB-2001
 2M0173G22F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC2M0173G22 F, genomic survey sequence.

DEFINITION

ACCESSION

AZ864022.1 GI:13062908

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0173 row: G column: 22

Seq primer: GTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0173G22"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

/note="Vector: Qiagen's pDrive; Messenger RNA was
 extracted from control and cold acclimated bermudagrass
 crown tissue at 2 and 28 days after acclimation and cDNA
 library was constructed following Clontech PCR- select
 cDNA subtraction procedure."

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:41:06 ; Search time 100 Seconds
(without alignments)
355.511 Million cell updates

Title: US-10-604-926A-4539

Perfect score:

Sequence: 1 ggagaaggggtgggtgct 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs. 935554401 residues

Total number of hits satisfying chosen parameters: 1097684

Minimum DB seq length: 0

Maximum DB seq length:	0
Maximum DB seq length:	30

Post-processing: Minimum March 0%

FOCUS-PROCESSING: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents NA.**

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1: /EMC Celerra_SIDS3/ptodata/2/ina/1_COMB.seq.*
2: /EMC Celerra_SIDS3/ptodata/2/ina/5_COMB.seq.*
3: /EMC Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq.*
4: /EMC Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq.*
5: /EMC Celerra_SIDS3/ptodata/2/ina/7_COMB.seq.*
6: /EMC Celerra_SIDS3/ptodata/2/ina/H_COMB.seq.*
7: /EMC Celerra_SIDS3/ptodata/2/ina/PPCTRUS_COMB.seq.*
8: /EMC Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq.*
9: /EMC Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq.*
10: /EMC Celerra_SIDS3/ptodata/2/ina/backfiles.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C 1	13.8	72.6	20	3	US-08-914-961-8	Sequence 8, Appli
C 2	13.4	70.5	22	3	US-10-085-612A-23	Sequence 23, Appli
C 3	13.2	69.5	18	3	US-09-422-978-9827	Sequence 9827, Ap
C 4	13.2	69.5	21	3	US-09-792-686A-21	Sequence 21, Appli
C 5	13.2	69.5	25	3	US-09-067-626-12	Sequence 12, Appli
C 6	12.8	67.4	27	2	US-08-173-489C-359	Sequence 359, App
C 7	12.6	66.3	25	3	US-08-943-731-424	Sequence 424, App
C 8	12.4	65.3	17	3	US-09-282-146-4	Sequence 4, Appli
C 9	12.4	65.3	18	3	US-09-205-921-33	Sequence 33, Appli
C 10	12.4	65.3	21	3	US-09-657-472-246	Sequence 246, App
C 11	12.4	65.3	22	3	US-08-927-219-64	Sequence 64, Appli
C 12	12.4	65.3	27	3	US-09-716-964B-191	Sequence 191, App
C 13	12.4	65.3	30	2	US-08-504-511A-6	Sequence 6, Appli
C 14	12.4	65.3	30	3	US-09-119-507B-38	Sequence 10, Appli
C 15	12.4	65.3	30	3	US-09-119-507B-38	Sequence 38, Appli
C 16	12.4	65.3	30	3	US-09-119-507B-39	Sequence 39, Appli
C 17	12.4	65.3	30	3	US-08-897-556A-10	Sequence 10, Appli
C 18	12.4	65.3	30	3	US-08-897-556A-38	Sequence 38, Appli
C 19	12.4	65.3	30	3	US-08-897-556A-39	Sequence 39, Appli
C 20	12.4	65.3	30	3	US-09-547-693-10	Sequence 10, Appli
C 21	12.4	65.3	30	3	US-09-547-693-38	Sequence 38, Appli
C 22	12.4	65.3	30	3	US-09-547-693-39	Sequence 39, Appli
C 23	12.2	64.2	18	2	US-08-531-555-122	Sequence 122, App

97	11.8	62.1	28	3	US-08-442-144A-74	Sequence 74, Appl	170	11.2	58.9	22	2	US-08-753-979A-24	Sequence 24, Appl
98	11.8	62.1	28	3	US-08-441-970-74	Sequence 74, Appl	171	11.2	58.9	22	2	US-08-753-979A-40	Sequence 40, Appl
99	11.8	62.1	30	3	US-09-733-271-1614	Sequence 1614, Ap	c 172	11.2	58.9	22	3	US-09-305-384-4	Sequence 4, Appl
100	11.6	61.1	18	5	US-10-006-069A-117	Sequence 117, App	c 173	11.2	58.9	22	4	US-09-441-857-42	Sequence 42, Appl
c 101	11.6	61.1	19	3	US-09-913-524-28	Sequence 28, Appl	174	11.2	58.9	23	3	US-09-167-681-10	Sequence 10, Appl
c 102	11.6	61.1	19	3	US-09-632-748-5	Sequence 5, Appl	175	11.2	58.9	23	3	US-09-851-896-6	Sequence 6, Appl
c 103	11.6	61.1	19	3	US-09-332-803A-44	Sequence 44, Appl	176	11.2	58.9	23	3	US-09-778-898A-2	Sequence 2, Appl
c 104	11.6	61.1	19	3	US-09-573-740A-25	Sequence 25, Appl	177	11.2	58.9	23	3	US-09-778-898A-6	Sequence 6, Appl
c 105	11.6	61.1	20	2	US-08-117-952-424	Sequence 424, App	178	11.2	58.9	24	2	US-07-832-905B-72	Sequence 72, Appl
c 106	11.6	61.1	20	3	US-09-522-775A-6	Sequence 6, Appl	c 179	11.2	58.9	24	2	US-08-598-591-18	Sequence 18, Appl
c 107	11.6	61.1	20	3	US-08-836-734E-43	Sequence 43, Appl	c 180	11.2	58.9	24	2	US-08-798-691-22	Sequence 22, Appl
c 108	11.6	61.1	20	3	US-09-906-158-34	Sequence 34, Appl	181	11.2	58.9	24	2	US-08-700-757-72	Sequence 72, Appl
c 109	11.6	61.1	24	3	US-09-820-182-9	Sequence 9, Appl	c 182	11.2	58.9	24	2	US-08-480-640A-127	Sequence 127, App
c 110	11.6	61.1	25	3	US-08-818-581B-2	Sequence 2, Appl	c 183	11.2	58.9	24	3	US-08-825-487A-22	Sequence 22, Appl
c 111	11.6	61.1	25	3	US-09-396-196G-115987	Sequence 115987,	c 184	11.2	58.9	24	3	US-08-295-802-127	Sequence 22, Appl
c 112	11.6	61.1	27	3	US-09-940-244-310	Sequence 310, App	c 185	11.2	58.9	24	3	US-09-074-476-22	Sequence 22, Appl
c 113	11.6	61.1	27	3	US-09-777-430C-40	Sequence 40, Appl	c 186	11.2	58.9	24	3	US-08-488-237A-127	Sequence 127, App
c 114	11.6	61.1	30	2	US-08-123-702-26	Sequence 26, Appl	c 187	11.2	58.9	24	3	US-08-375-992A-127	Sequence 127, App
c 115	11.4	60.0	14	3	US-09-808-457-10	Sequence 10, Appl	188	11.2	58.9	24	3	US-09-123-728-3	Sequence 3, Appl
c 116	11.4	60.0	17	3	US-09-360-416-6	Sequence 6, Appl	c 189	11.2	58.9	24	3	US-08-472-679H-127	Sequence 127, App
c 117	11.4	60.0	17	3	US-10-175-225-6	Sequence 6, Appl	c 190	11.2	58.9	24	3	US-08-734-672A-22	Sequence 22, Appl
c 118	11.4	60.0	20	2	US-08-828-511-16	Sequence 16, Appl	c 191	11.2	58.9	24	3	US-09-923-327A-88	Sequence 88, Appl
c 119	11.4	60.0	20	3	US-09-198-452A-6205	Sequence 6205, Ap	192	11.2	58.9	25	2	US-08-495-743-63	Sequence 63, Appl
c 120	11.4	60.0	20	3	US-09-198-452A-6208	Sequence 6208, Ap	193	11.2	58.9	25	2	US-08-495-739-63	Sequence 63, Appl
c 121	11.4	60.0	20	3	US-09-904-420A-8	Sequence 8, Appl	194	11.2	58.9	25	2	US-08-495-741-63	Sequence 63, Appl
c 122	11.4	60.0	20	7	PCT-US94-04361-9	Sequence 9, Appl	195	11.2	58.9	25	3	US-08-062-023-63	Sequence 63, Appl
c 123	11.4	60.0	22	3	US-08-891-271-23	Sequence 23, Appl	c 196	11.2	58.9	25	3	US-10-766-190-15	Sequence 15, Appl
c 124	11.4	60.0	22	3	US-09-018-138-15	Sequence 15, Appl	c 197	11.2	58.9	25	3	US-08-675-828A-63	Sequence 63, Appl
c 125	11.4	60.0	22	3	US-08-890-929-3	Sequence 3, Appl	c 198	11.2	58.9	26	2	US-08-859-998-532	Sequence 532, App
c 126	11.4	60.0	22	3	US-09-959-007-3	Sequence 3, Appl	c 199	11.2	58.9	26	2	US-09-225-928-532	Sequence 532, App
c 127	11.4	60.0	23	3	US-09-149-922-47	Sequence 47, Appl	c 200	11.2	58.9	26	3	US-09-225-201B-532	Sequence 532, App
c 128	11.4	60.0	24	3	US-09-999-833A-239	Sequence 239, App	201	11.2	58.9	27	3	US-09-678-300-21	Sequence 21, Appl
c 129	11.4	60.0	24	3	US-10-020-445A-239	Sequence 239, App	202	11.2	58.9	27	3	US-09-255-518C-30	Sequence 30, Appl
c 130	11.4	60.0	24	4	US-09-978-189-239	Sequence 239, App	c 203	11.2	58.9	27	3	US-09-791-500-28	Sequence 28, Appl
c 131	11.4	60.0	24	4	US-10-017-085A-239	Sequence 239, App	c 204	11.2	58.9	27	3	US-09-619-380-10	Sequence 10, Appl
c 132	11.4	60.0	24	5	US-10-145-129A-239	Sequence 239, App	205	11.2	58.9	27	5	US-09-762-278-13	Sequence 13, Appl
c 133	11.4	60.0	24	5	US-10-013-929A-239	Sequence 239, App	c 206	11.2	58.9	27	5	US-10-655-073-10	Sequence 10, Appl
c 134	11.4	60.0	24	5	US-10-013-917A-239	Sequence 239, App	207	11.2	58.9	30	3	US-08-384-708A-145	Sequence 145, App
c 135	11.4	60.0	26	3	US-09-367-513-8	Sequence 8, Appl	208	11.2	58.9	30	3	US-08-687-421-145	Sequence 145, App
c 136	11.4	60.0	27	3	US-08-948-113D-15	Sequence 15, Appl	209	11.2	58.9	30	3	US-08-442-423-145	Sequence 145, App
c 137	11.4	60.0	27	3	US-08-815-923-19	Sequence 19, Appl	210	11	57.9	11	2	US-08-231-193A-9	Sequence 9, Appl
c 138	11.4	60.0	28	2	US-08-928-692-7	Sequence 7, Appl	211	11	57.9	11	2	US-08-486-273A-9	Sequence 9, Appl
c 139	11.4	60.0	28	3	US-09-339-972-7	Sequence 7, Appl	212	11	57.9	11	3	US-08-480-474-9	Sequence 9, Appl
c 140	11.4	60.0	29	3	US-09-304-232-552	Sequence 552, App	213	11	57.9	11	3	US-08-940-086A-9	Sequence 9, Appl
c 141	11.4	60.0	29	3	US-09-848-537A-24	Sequence 24, Appl	214	11	57.9	11	3	US-08-940-035A-9	Sequence 9, Appl
c 142	11.4	60.0	29	3	US-09-775-743C-30	Sequence 30, Appl	215	11	57.9	11	3	US-08-935-105A-9	Sequence 9, Appl
c 143	11.4	60.0	29	3	US-09-932-812A-1	Sequence 1, Appl	216	11	57.9	11	3	US-09-648-797-9	Sequence 9, Appl
c 144	11.4	60.0	30	3	US-11-016-518A-1	Sequence 41, Appl	217	11	57.9	11	3	US-09-386-123-9	Sequence 9, Appl
c 145	11.4	60.0	30	3	US-09-733-042-41	Sequence 41, Appl	218	11	57.9	11	3	US-10-007-747-9	Sequence 9, Appl
c 146	11.2	58.9	17	5	US-10-156-306B-3651	Sequence 3651, Ap	219	11	57.9	11	3	US-09-945-901-9	Sequence 9, Appl
c 147	11.2	58.9	19	2	US-08-473-096-17	Sequence 17, Appl	220	11	57.9	11	2	US-08-173-489C-261	Sequence 261, App
c 148	11.2	58.9	20	2	US-08-136-811-15	Sequence 15, Appl	221	11	57.9	12	2	US-08-173-489C-261	Sequence 261, App
c 149	11.2	58.9	20	2	US-08-031-147A-49	Sequence 49, Appl	222	11	57.9	13	2	US-08-233-002A-1	Sequence 1, Appl
c 150	11.2	58.9	20	2	US-08-487-141B-82	Sequence 82, Appl	c 223	11	57.9	19	2	US-08-953-290-1	Sequence 1, Appl
c 151	11.2	58.9	20	2	US-08-487-141B-83	Sequence 83, Appl	c 224	11	57.9	19	3	US-08-224-232A-1	Sequence 1, Appl
c 152	11.2	58.9	20	2	US-08-835-770-15	Sequence 15, Appl	c 225	11	57.9	19	3	US-08-145-826A-1	Sequence 1, Appl
c 153	11.2	58.9	20	2	US-08-628-731-15	Sequence 15, Appl	c 226	11	57.9	19	3	US-09-668-532-1	Sequence 1, Appl
c 154	11.2	58.9	20	2	US-08-927-561-82	Sequence 82, Appl	c 227	11	57.9	19	3	US-09-580-043B-6	Sequence 6, Appl
c 155	11.2	58.9	20	3	US-09-166-186-133	Sequence 133, App	c 228	11	57.9	19	3	US-08-459-713-1	Sequence 1, Appl
c 156	11.2	58.9	20	3	US-09-429-322-56	Sequence 56, Appl	c 229	11	57.9	19	3	US-08-918-407-1	Sequence 1, Appl
c 157	11.2	58.9	20	3	US-09-313-932-133	Sequence 133, App	c 230	11	57.9	19	3	US-09-413-109-1	Sequence 1, Appl
c 158	11.2	58.9	20	3	US-09-422-978-9212	Sequence 9212, Ap	c 231	11	57.9	19	3	US-10-180-895-1	Sequence 1, Appl
c 159	11.2	58.9	20	7	PCT-US94-02471-49	Sequence 49, Appl	c 232	11	57.9	19	3	US-08-626-678-1	Sequence 1, Appl
c 160	11.2	58.9	20	7	PCT-US96-09388-82	Sequence 82, Appl	c 233	11	57.9	19	5	US-10-170-240-1	Sequence 1, Appl
c 161	11.2	58.9	20	7	PCT-US96-09388-82	Sequence 82, Appl	c 234	11	57.9	20	3	US-09-166-186-131	Sequence 131, App
c 162	11.2	58.9	21	2	US-08-440-787A-39	Sequence 39, Appl	c 235	11	57.9	20	3	US-09-313-932A-1	Sequence 21, App
c 163	11.2	58.9	21	2	US-08-367-685-39	Sequence 39, Appl	c 236	11	57.9	20	3	US-09-721-832A-21	Sequence 21, Appl
c 164	11.2	58.9	21	3	US-09-109-663-4	Sequence 4, Appl	c 237	11	57.9	20	3	US-09-721-832A-22	Sequence 22, Appl
c 165	11.2	58.9	21	3	US-09-657-472-1486	Sequence 1486, Ap	c 238	11	57.9	20	3	US-09-980-052-89	Sequence 89, Appl
c 166	11.2	58.9	21	7	PCT-US91-07141-39	Sequence 39, Appl	239	11	57.9	20	3	US-10-002-623-120	Sequence 120, App
c 167	11.2	58.9	22	2	US-08-531-556-98	Sequence 98, Appl	240	11	57.9	20	3	US-10-002-623-120	Sequence 120, App
c 168	11.2	58.9	22	2	US-08-753-979A-10	Sequence 10, Appl	241	11	57.9	21	3	US-08-469-318-103	Sequence 103, App
c 169	11.2	58.9	22	2			242	11	57.9	21	3	US-08-468-609A-103	Sequence 103, App

243	11	57.9	21	3	US-09-311-912-6	Sequence 6, Appli	Sequence 6, Appli	Sequence 5568, Ap
244	11	57.9	21	3	US-08-737-061-4	Sequence 4, Appli	Sequence 74, Appl	
245	11	57.9	21	3	US-08-446-872A-103	Sequence 103, App	Sequence 322, App	
246	11	57.9	21	3	US-08-762-227A-103	Sequence 103, App	Sequence 322, App	
247	11	57.9	21	3	US-09-510-238A-74	Sequence 74, Appl	Sequence 33, Appl	
248	11	57.9	21	3	US-09-158-272-4	Sequence 4, Appli	Sequence 4, Appli	
249	11	57.9	21	3	US-09-269-717-8	Sequence 8, Appli	Sequence 27, Appl	
250	11	57.9	21	3	US-08-957-610A-378	Sequence 378, App	Sequence 5, Appli	
251	11	57.9	21	7	PCT-US95-01185-103	Sequence 103, App	Sequence 24, Appl	
252	11	57.9	22	2	US-08-332-766A-69	Sequence 69, Appl	Sequence 5, Appli	
253	11	57.9	24	3	US-09-090-535-14	Sequence 14, Appl	Sequence 24, Appl	
254	11	57.9	25	2	US-08-495-743-47	Sequence 47, Appl	Sequence 102, App	
255	11	57.9	25	2	US-08-495-743-47	Sequence 47, Appl	Sequence 11, Appl	
256	11	57.9	25	2	US-08-495-741-47	Sequence 47, Appl	Sequence 11, Appl	
257	11	57.9	25	2	US-08-469-318-104	Sequence 104, App	Sequence 30, Appl	
258	11	57.9	25	3	US-08-468-609A-104	Sequence 104, App	Sequence 142, App	
259	11	57.9	25	3	US-08-062-023-47	Sequence 47, Appl	Sequence 142, App	
260	11	57.9	25	3	US-08-446-872A-104	Sequence 104, App	Sequence 142, App	
261	11	57.9	25	3	US-08-762-227A-104	Sequence 104, App	Sequence 142, App	
262	11	57.9	25	3	US-09-787-628-7	Sequence 7, Appli	Sequence 142, App	
263	11	57.9	25	3	US-08-062-021A-2	Sequence 2, Appli	Sequence 142, App	
264	11	57.9	25	3	US-09-510-238A-75	Sequence 75, Appl	Sequence 142, App	
265	11	57.9	25	3	US-09-721-543A-33	Sequence 33, Appl	Sequence 142, App	
266	11	57.9	25	3	US-09-721-543A-40	Sequence 40, Appl	Sequence 142, App	
267	11	57.9	25	3	US-09-675-828A-47	Sequence 47, Appl	Sequence 142, App	
268	11	57.9	25	4	US-08-957-610A-379	Sequence 379, App	Sequence 142, App	
269	11	57.9	25	7	PCT-US95-01185-104	Sequence 104, App	Sequence 142, App	
270	11	57.9	26	3	US-09-926-169-4	Sequence 4, Appli	Sequence 142, App	
271	11	57.9	27	2	US-07-938-334C-10	Sequence 10, Appl	Sequence 1, Appli	
272	11	57.9	27	2	US-08-145-704-14	Sequence 14, Appl	Sequence 1, Appli	
273	11	57.9	27	3	US-08-587-574-14	Sequence 14, Appl	Sequence 15, Appl	
274	11	57.9	27	3	US-08-535-168-14	Sequence 14, Appl	Sequence 15, Appl	
275	11	57.9	27	3	US-09-017-974-14	Sequence 14, Appl	Sequence 15, Appl	
276	11	57.9	27	3	US-08-682-255A-14	Sequence 14, Appl	Sequence 15, Appl	
277	11	57.9	27	3	US-09-429-130-14	Sequence 14, Appl	Sequence 15, Appl	
278	11	57.9	27	3	US-09-409-648-14	Sequence 14, Appl	Sequence 15, Appl	
279	11	57.9	27	5	US-09-543-679A-1441	Sequence 1441, Ap	Sequence 15, Appl	
280	11	57.9	27	7	PCT-US96-11786-14	Sequence 14, Appl	Sequence 15, Appl	
281	11	57.9	28	3	US-09-152-361A-14	Sequence 14, Appl	Sequence 15, Appl	
282	11	57.9	29	3	US-09-304-232-367	Sequence 367, App	Sequence 15, Appl	
283	11	57.9	29	3	US-09-304-232-553	Sequence 553, App	Sequence 15, Appl	
284	11	57.9	29	3	US-09-647-841B-4	Sequence 4, Appli	Sequence 15, Appl	
285	11	57.9	29	3	US-09-647-841B-5	Sequence 5, Appli	Sequence 15, Appl	
286	11	57.9	29	3	US-08-592-406-27	Sequence 27, Appl	Sequence 15, Appl	
287	10.8	56.8	14	4	US-09-601-326-157	Sequence 157, App	Sequence 12, Appl	
288	10.8	56.8	14	4	US-10-428-826-157	Sequence 157, App	Sequence 12, Appl	
289	10.8	56.8	15	2	US-08-479-248-1	Sequence 1, Appli	Sequence 12, Appl	
290	10.8	56.8	15	2	US-08-479-248-2	Sequence 2, Appli	Sequence 12, Appl	
291	10.8	56.8	15	3	US-08-557-210A-1	Sequence 1, Appli	Sequence 12, Appl	
292	10.8	56.8	15	3	US-08-557-210A-2	Sequence 2, Appli	Sequence 12, Appl	
293	10.8	56.8	17	2	US-08-390-850-591	Sequence 591, App	Sequence 12, Appl	
294	10.8	56.8	17	2	US-08-373-124A-178	Sequence 178, App	Sequence 12, Appl	
295	10.8	56.8	17	2	US-08-435-634-591	Sequence 591, App	Sequence 12, Appl	
296	10.8	56.8	17	2	US-08-435-628-178	Sequence 178, App	Sequence 12, Appl	
297	10.8	56.8	17	3	US-09-474-432B-855	Sequence 855, App	Sequence 12, Appl	
298	10.8	56.8	17	3	US-09-476-387-854	Sequence 854, App	Sequence 12, Appl	
299	10.8	56.8	17	3	US-09-866-108A-2312	Sequence 2312, Ap	Sequence 12, Appl	
300	10.8	56.8	17	3	US-09-866-108A-2313	Sequence 2313, Ap	Sequence 12, Appl	
301	10.8	56.8	17	3	US-09-866-108A-2314	Sequence 2314, Ap	Sequence 12, Appl	
302	10.8	56.8	17	3	US-09-866-108A-2315	Sequence 2315, Ap	Sequence 12, Appl	
303	10.8	56.8	17	3	US-09-866-108A-6789	Sequence 6789, Ap	Sequence 12, Appl	
304	10.8	56.8	17	3	US-09-866-108A-6793	Sequence 6793, Ap	Sequence 12, Appl	
305	10.8	56.8	17	4	US-10-222-825-6	Sequence 6, Appli	Sequence 12, Appl	
306	10.8	56.8	18	3	US-09-544-398B-475	Sequence 475, App	Sequence 12, Appl	
307	10.8	56.8	18	3	US-09-543-771B-475	Sequence 475, App	Sequence 12, Appl	
308	10.8	56.8	18	4	US-09-331-204A-5	Sequence 5, Appli	Sequence 12, Appl	
309	10.8	56.8	18	4	US-09-331-204A-20	Sequence 20, Appl	Sequence 12, Appl	
310	10.8	56.8	19	3	US-08-422-978-6862	Sequence 6862, Ap	Sequence 12, Appl	
311	10.8	56.8	20	2	US-08-263-413-11	Sequence 11, Appl	Sequence 12, Appl	
312	10.8	56.8	20	3	US-09-433-694-20	Sequence 20, Appl	Sequence 12, Appl	
313	10.8	56.8	20	3	US-09-490-692-123	Sequence 123, App	Sequence 12, Appl	
314	10.8	56.8	20	3	US-09-658-688A-47	Sequence 47, Appl	Sequence 12, Appl	
315	10.8	56.8	20	3	US-09-198-452A-4824	Sequence 4824, Ap	Sequence 12, Appl	

389	10.6	55.8	17	7	PCT-US94-02471-34	Sequence 34, Appl	462	10.6	55.8	24	3	US-09-918-686-96	Sequence 96, Appl
390	10.6	55.8	18	3	US-09-216-393B-147	Sequence 147, App	463	10.6	55.8	24	3	US-08-559-390-437	Sequence 437, App
c 391	10.6	55.8	19	3	US-09-373-318-27	Sequence 27, Appl	464	10.6	55.8	24	3	US-08-899-112B-3	Sequence 3, Appl
c 392	10.6	55.8	19	3	US-09-696-791-3414	Sequence 3414, Ap	c 465	10.6	55.8	24	3	US-09-786-569-5	Sequence 5, Appl
393	10.6	55.8	20	2	US-08-031-147A-6	Sequence 6, Appl	466	10.6	55.8	24	3	US-10-106-275-13	Sequence 13, Appl
394	10.6	55.8	20	2	US-08-031-147A-11	Sequence 11, Appl	467	10.6	55.8	24	3	US-09-011-553-10	Sequence 10, Appl
395	10.6	55.8	20	2	US-08-031-147A-12	Sequence 12, Appl	468	10.6	55.8	24	5	US-10-007-132-20	Sequence 20, Appl
c 396	10.6	55.8	20	2	US-08-089-996-1	Sequence 1, Appl	469	10.6	55.8	24	5	US-10-007-132-33	Sequence 33, Appl
c 397	10.6	55.8	20	2	US-08-171-718-3	Sequence 3, Appl	470	10.6	55.8	24	7	PCT-US93-11198-437	Sequence 437, App
c 398	10.6	55.8	20	2	US-08-525-697-9	Sequence 9, Appl	471	10.6	55.8	25	3	US-08-822-440-30	Sequence 30, Appl
c 399	10.6	55.8	20	2	US-08-557-139-28	Sequence 28, Appl	472	10.6	55.8	25	3	US-09-396-540-30	Sequence 30, Appl
c 400	10.6	55.8	20	2	US-08-478-178A-1	Sequence 1, Appl	c 473	10.6	55.8	25	3	US-09-402-631A-27	Sequence 27, Appl
c 401	10.6	55.8	20	2	US-08-488-177-1	Sequence 1, Appl	474	10.6	55.8	25	3	US-09-396-196G-23085	Sequence 23085, A
c 402	10.6	55.8	20	2	US-08-481-072A-1	Sequence 1, Appl	c 475	10.6	55.8	25	3	US-09-396-196G-23385	Sequence 23385, A
c 403	10.6	55.8	20	2	US-08-664-336-1	Sequence 1, Appl	c 476	10.6	55.8	25	3	US-09-396-196G-28220	Sequence 28220, A
c 404	10.6	55.8	20	2	US-08-403-888A-21	Sequence 21, Appl	c 477	10.6	55.8	25	3	US-09-396-196G-36400	Sequence 36400, A
405	10.6	55.8	20	2	US-08-403-888A-127	Sequence 127, App	c 478	10.6	55.8	25	3	US-09-396-196G-37039	Sequence 37039, A
406	10.6	55.8	20	2	US-08-403-888A-128	Sequence 128, App	c 479	10.6	55.8	25	3	US-09-396-196G-37040	Sequence 37040, A
c 407	10.6	55.8	20	2	US-08-481-066A-1	Sequence 1, Appl	c 480	10.6	55.8	25	3	US-09-396-196G-51781	Sequence 51781, A
c 408	10.6	55.8	20	2	US-08-476-712-2	Sequence 2, Appl	481	10.6	55.8	25	3	US-09-396-196G-58972	Sequence 58972, A
c 409	10.6	55.8	20	3	US-08-578-615A-1	Sequence 1, Appl	482	10.6	55.8	25	3	US-09-396-196G-96021	Sequence 96021, A
c 410	10.6	55.8	20	3	US-08-578-615A-120	Sequence 120, App	c 483	10.6	55.8	25	3	US-09-396-196G-113561	Sequence 113561, A
c 411	10.6	55.8	20	3	US-08-478-087-3	Sequence 3, Appl	c 484	10.6	55.8	25	3	US-09-396-196G-113562	Sequence 113562, A
c 412	10.6	55.8	20	3	US-09-428-696-31	Sequence 31, Appl	c 485	10.6	55.8	25	3	US-09-396-196G-113563	Sequence 113563, A
c 413	10.6	55.8	20	3	US-09-031-006-12	Sequence 12, Appl	486	10.6	55.8	26	3	US-09-268-163-26	Sequence 26, Appl
c 414	10.6	55.8	20	3	US-09-225-749-1	Sequence 1, Appl	c 487	10.6	55.8	26	3	US-10-012-231A-452	Sequence 452, App
c 415	10.6	55.8	20	3	US-09-411-231-2	Sequence 2, Appl	c 488	10.6	55.8	26	3	US-09-622-745B-22	Sequence 22, Appl
c 416	10.6	55.8	20	3	US-08-829-637A-1	Sequence 1, Appl	c 489	10.6	55.8	26	3	US-09-622-745B-23	Sequence 23, Appl
c 417	10.6	55.8	20	3	US-09-851-520-19	Sequence 19, Appl	c 490	10.6	55.8	26	3	US-10-015-389A-452	Sequence 452, App
c 418	10.6	55.8	20	3	US-08-802-331-31	Sequence 31, Appl	c 491	10.6	55.8	26	3	US-10-006-768A-452	Sequence 452, App
c 419	10.6	55.8	20	3	US-09-806-254-14	Sequence 14, Appl	c 492	10.6	55.8	26	3	US-10-015-671A-452	Sequence 452, App
c 420	10.6	55.8	20	3	US-09-254-322-1	Sequence 1, Appl	c 493	10.6	55.8	26	3	US-10-015-393A-452	Sequence 452, App
c 421	10.6	55.8	20	3	US-10-025-139-1	Sequence 1, Appl	c 494	10.6	55.8	26	3	US-10-011-833A-452	Sequence 452, App
c 422	10.6	55.8	20	3	US-09-780-045-31	Sequence 31, Appl	c 495	10.6	55.8	26	3	US-10-006-041A-452	Sequence 452, App
423	10.6	55.8	20	3	US-09-922-271-12	Sequence 12, Appl	c 496	10.6	55.8	26	3	US-10-012-064A-452	Sequence 452, App
424	10.6	55.8	20	3	US-09-845-917-1	Sequence 10, Appl	c 497	10.6	55.8	26	4	US-10-015-795B-452	Sequence 452, App
c 425	10.6	55.8	20	3	US-09-864-894C-10	Sequence 10, Appl	c 498	10.6	55.8	26	5	US-10-011-795B-452	Sequence 452, App
c 426	10.6	55.8	20	3	US-09-864-894C-11	Sequence 11, Appl	499	10.6	55.8	26	5	US-10-033-026-26	Sequence 26, Appl
c 427	10.6	55.8	20	3	US-09-863-049B-49	Sequence 49, Appl	c 500	10.6	55.8	26	5	US-10-015-386A-452	Sequence 452, App
c 428	10.6	55.8	20	3	US-09-269-446D-49	Sequence 49, Appl	c 501	10.6	55.8	26	5	US-10-012-121A-452	Sequence 452, App
c 429	10.6	55.8	20	7	PCT-US93-02213-1	Sequence 1, Appl	c 502	10.6	55.8	26	5	US-10-006-485A-452	Sequence 452, App
430	10.6	55.8	20	7	PCT-US94-02471-6	Sequence 6, Appl	c 503	10.6	55.8	26	5	US-10-006-746A-452	Sequence 452, App
431	10.6	55.8	20	7	PCT-US94-02471-11	Sequence 11, Appl	c 504	10.6	55.8	26	5	US-10-012-752A-452	Sequence 452, App
432	10.6	55.8	20	7	PCT-US94-02471-12	Sequence 12, Appl	c 505	10.6	55.8	26	5	US-10-017-253A-452	Sequence 452, App
c 433	10.6	55.8	20	7	PCT-US94-07770-1	Sequence 1, Appl	c 506	10.6	55.8	26	5	US-10-015-519A-452	Sequence 452, App
434	10.6	55.8	21	3	US-08-594-452-78	Sequence 78, Appl	c 507	10.6	55.8	26	5	US-10-015-715A-452	Sequence 452, App
435	10.6	55.8	21	3	US-09-258-408-78	Sequence 78, Appl	c 508	10.6	55.8	27	2	US-10-007-236A-452	Sequence 452, App
436	10.6	55.8	21	3	US-09-230-704-9	Sequence 9, Appl	c 509	10.6	55.8	27	3	US-07-807-529A-54	Sequence 54, Appl
437	10.6	55.8	21	3	US-09-609-162-9	Sequence 9, Appl	c 510	10.6	55.8	27	3	US-08-513-974B-163	Sequence 163, App
438	10.6	55.8	21	3	US-09-634-732-9	Sequence 9, Appl	511	10.6	55.8	27	3	US-09-164-210-14	Sequence 14, Appl
c 439	10.6	55.8	21	3	US-09-859-053-9	Sequence 9, Appl	512	10.6	55.8	28	3	US-09-197-218-5	Sequence 5, Appl
c 440	10.6	55.8	21	3	US-10-048-882C-11	Sequence 11, Appl	513	10.6	55.8	29	3	US-08-840-062-13	Sequence 13, Appl
c 441	10.6	55.8	21	5	US-10-349-852-5	Sequence 5, Appl	c 514	10.6	55.8	29	3	US-08-462-941-24	Sequence 24, Appl
c 442	10.6	55.8	22	3	US-08-974-549A-496	Sequence 496, App	515	10.6	55.8	30	2	US-08-467-126-1	Sequence 1, Appl
c 443	10.6	55.8	22	3	US-09-203-895-8	Sequence 8, Appl	516	10.6	55.8	30	2	US-08-476-712-3	Sequence 3, Appl
c 444	10.6	55.8	22	3	US-08-912-951-263	Sequence 263, App	c 517	10.6	55.8	30	3	US-08-341-560B-30	Sequence 30, Appl
c 445	10.6	55.8	22	3	US-09-402-181B-496	Sequence 496, App	518	10.6	55.8	30	3	US-08-983-075D-2	Sequence 2, Appl
c 446	10.6	55.8	22	3	US-09-721-456-496	Sequence 496, App	519	10.6	55.8	30	3	US-09-411-291-3	Sequence 3, Appl
c 447	10.6	55.8	22	3	US-09-283-909-14	Sequence 14, Appl	520	10.6	55.8	30	3	US-09-052-919-50	Sequence 50, Appl
c 448	10.6	55.8	22	4	US-09-762-278-9	Sequence 9, Appl	521	10.6	55.8	30	3	US-09-953-052-50	Sequence 50, Appl
c 449	10.6	55.8	23	2	US-08-347-343-1	Sequence 1, Appl	522	10.6	55.8	30	10	5245022-25	Patent No. 5245022
450	10.6	55.8	23	3	US-07-808-452-15	Sequence 15, Appl	c 523	10.4	54.7	13	2	US-08-250-740-31	Sequence 31, Appl
451	10.6	55.8	23	7	PCT-US92-10770-15	Sequence 15, Appl	c 524	10.4	54.7	14	3	US-09-328-174A-20	Sequence 20, Appl
452	10.6	55.8	23	7	PCT-US92-10792-13	Sequence 13, Appl	c 525	10.4	54.7	17	2	US-08-250-740-13	Sequence 13, Appl
453	10.6	55.8	24	2	US-08-411-796-437	Sequence 437, App	c 526	10.4	54.7	17	3	US-09-686-597-21	Sequence 21, Appl
454	10.6	55.8	24	2	US-08-626-685A-3	Sequence 3, Appl	527	10.4	54.7	17	3	US-09-866-108A-6787	Sequence 6787, Ap
455	10.6	55.8	24	3	US-08-594-452-79	Sequence 79, App	528	10.4	54.7	17	3	US-09-866-108A-6788	Sequence 6788, Ap
456	10.6	55.8	24	3	US-08-471-039-437	Sequence 437, App	c 529	10.4	54.7	18	3	US-09-493-565-7	Sequence 7, Appl
457	10.6	55.8	24	3	US-09-258-408-79	Sequence 79, Appl	530	10.4	54.7	18	3	US-09-432-177A-7812	Sequence 7812, Ap
458	10.6	55.8	24	3	US-09-199-737-20	Sequence 20, Appl	c 531	10.4	54.7	19	2	US-08-222-177A-299	Sequence 299, App
459	10.6	55.8	24	3	US-09-199-737-33	Sequence 33, Appl	532	10.4	54.7	19	2	US-08-631-200-47	Sequence 47, Appl
460	10.6	55.8	24	3	US-09-058-333A-20	Sequence 20, Appl	533	10.4	54.7	19	2	US-08-829-553-47	Sequence 47, Appl
461	10.6	55.8	24	3	US-09-058-333A-33	Sequence 33, Appl	534	10.4	54.7	19	2	US-08-922-267A-47	Sequence 47, Appl

535	10.4	54.7	19	2	US-08-936-707A-47	Sequence 47, Appl	c 608	10.2	53.7	17	3	US-09-371-772B-2368	Sequence 2368, Ap
536	10.4	54.7	19	2	US-08-936-706A-47	Sequence 47, Appl	609	10.2	53.7	17	3	US-09-476-387-820	Sequence 820, App
537	10.4	54.7	19	2	US-09-248-203-47	Sequence 47, Appl	c 610	10.2	53.7	17	3	US-09-476-387-838	Sequence 838, App
538	10.4	54.7	19	3	US-09-406-071-47	Sequence 47, Appl	611	10.2	53.7	17	3	US-09-866-108A-895	Sequence 895, App
539	10.4	54.7	19	3	US-09-814-986-47	Sequence 47, Appl	612	10.2	53.7	17	3	US-09-866-108A-896	Sequence 896, App
c 540	10.4	54.7	19	3	US-10-164-230-59	Sequence 59, Appl	613	10.2	53.7	17	3	US-09-866-108A-897	Sequence 26, Appl
c 541	10.4	54.7	20	2	US-08-487-141B-63	Sequence 22, Appl	614	10.2	53.7	17	3	US-10-059-877-26	Sequence 26, Appl
c 542	10.4	54.7	20	2	US-08-512-681-22	Sequence 22, Appl	c 615	10.2	53.7	17	3	US-09-685-664B-2368	Sequence 2368, Ap
c 543	10.4	54.7	20	2	US-08-927-561-63	Sequence 63, Appl	616	10.2	53.7	17	5	US-10-156-306B-3652	Sequence 3652, Ap
544	10.4	54.7	20	3	US-08-991-426-15	Sequence 15, Appl	617	10.2	53.7	17	5	US-10-156-306B-3652	Sequence 3652, Ap
545	10.4	54.7	20	3	US-09-143-470-11	Sequence 11, Appl	c 618	10.2	53.7	17	5	US-10-138-674B-2368	Sequence 2368, Ap
546	10.4	54.7	20	3	US-08-753-007A-30	Sequence 30, Appl	619	10.2	53.7	18	2	US-08-424-663-6	Sequence 6, Appl
547	10.4	54.7	20	3	US-09-398-496-30	Sequence 30, Appl	c 620	10.2	53.7	18	2	US-08-311-486C-1060	Sequence 1060, Ap
548	10.4	54.7	20	3	US-09-052-995-13	Sequence 13, Appl	c 621	10.2	53.7	18	2	US-08-311-486C-1143	Sequence 1143, Ap
549	10.4	54.7	20	3	US-09-536-259-9	Sequence 9, Appl	622	10.2	53.7	18	2	US-08-529-878B-3	Sequence 3, Appl
550	10.4	54.7	20	3	US-09-980-052-81	Sequence 81, Appl	623	10.2	53.7	18	2	US-08-529-878B-44	Sequence 44, Appl
551	10.4	54.7	20	3	US-09-856-371A-27	Sequence 27, Appl	624	10.2	53.7	18	2	US-08-726-012B-8	Sequence 8, Appl
c 552	10.4	54.7	20	3	US-10-002-623-23	Sequence 23, Appl	625	10.2	53.7	18	2	US-09-161-015-45	Sequence 45, Appl
c 553	10.4	54.7	20	7	PCR-US966-09388-63	Sequence 63, Appl	626	10.2	53.7	18	2	US-08-872-446-6	Sequence 6, Appl
c 554	10.4	54.7	21	3	US-09-382-552-185	Sequence 185, App	c 627	10.2	53.7	18	2	US-08-872-446-10	Sequence 10, Appl
555	10.4	54.7	21	3	US-09-657-472-1426	Sequence 1426, Ap	628	10.2	53.7	18	3	US-09-280-409-58	Sequence 58, Appl
556	10.4	54.7	22	3	US-09-745-129-2	Sequence 2, Appl	c 629	10.2	53.7	18	3	US-09-025-701-4	Sequence 4, Appl
c 557	10.4	54.7	23	3	US-08-849-602C-14	Sequence 14, Appl	c 630	10.2	53.7	18	3	US-09-630-706-55	Sequence 55, Appl
c 558	10.4	54.7	23	3	US-09-046-894-14	Sequence 14, Appl	631	10.2	53.7	18	3	US-09-280-270A-6	Sequence 6, Appl
559	10.4	54.7	24	3	US-09-255-518C-37	Sequence 37, Appl	c 632	10.2	53.7	18	3	US-09-280-270A-10	Sequence 10, Appl
c 560	10.4	54.7	24	3	US-10-112-802-14	Sequence 14, Appl	c 633	10.2	53.7	18	3	US-09-167-109-34	Sequence 34, Appl
c 561	10.4	54.7	24	3	US-10-112-802-18	Sequence 18, Appl	634	10.2	53.7	18	3	US-09-387-341-188	Sequence 188, App
c 562	10.4	54.7	24	3	US-09-981-953A-13	Sequence 13, Appl	635	10.2	53.7	18	3	US-09-725-265-46	Sequence 46, Appl
563	10.4	54.7	25	3	US-09-866-108A-11679	Sequence 11679, A	c 636	10.2	53.7	18	3	US-09-725-265-50	Sequence 50, Appl
564	10.4	54.7	25	3	US-09-866-108A-11680	Sequence 11680, A	c 637	10.2	53.7	18	3	US-09-422-978-7437	Sequence 7437, Ap
c 565	10.4	54.7	25	3	US-09-396-196G-75137	Sequence 75137, A	c 638	10.2	53.7	18	3	US-09-663-834A-41	Sequence 41, Appl
566	10.4	54.7	25	3	US-09-396-196G-118171	Sequence 118171, A	c 639	10.2	53.7	18	3	US-09-556-127-46	Sequence 46, Appl
567	10.4	54.7	26	2	US-09-971-773-69	Sequence 69, Appl	c 640	10.2	53.7	18	3	US-09-556-127-50	Sequence 50, Appl
568	10.4	54.7	26	2	US-08-254-114A-3	Sequence 3, Appl	c 641	10.2	53.7	18	4	US-09-331-204A-4	Sequence 4, Appl
569	10.4	54.7	26	2	US-08-721-260-12	Sequence 12, Appl	642	10.2	53.7	18	4	US-09-331-204A-8	Sequence 8, Appl
570	10.4	54.7	26	3	US-08-818-082-1	Sequence 1, Appl	643	10.2	53.7	19	3	US-08-860-038-6	Sequence 6, Appl
571	10.4	54.7	26	3	US-08-997-685A-26	Sequence 26, Appl	644	10.2	53.7	19	3	US-09-580-923-6	Sequence 6, Appl
572	10.4	54.7	26	3	US-09-692-056-1	Sequence 1, Appl	c 645	10.2	53.7	19	3	US-09-387-341-198	Sequence 198, App
573	10.4	54.7	27	2	US-08-410-654B-44	Sequence 44, Appl	646	10.2	53.7	19	3	US-09-153-838-10	Sequence 10, Appl
574	10.4	54.7	27	2	US-08-478-851-44	Sequence 44, Appl	c 647	10.2	53.7	19	3	US-09-975-123-4	Sequence 4, Appl
575	10.4	54.7	27	2	US-08-481-560-44	Sequence 44, Appl	648	10.2	53.7	19	3	US-09-696-731-528	Sequence 528, App
576	10.4	54.7	27	2	US-08-607-509-13	Sequence 13, Appl	649	10.2	53.7	19	10	5352575-10	Patent No. 5352575
577	10.4	54.7	27	2	US-08-634-642-13	Sequence 13, Appl	650	10.2	53.7	20	2	US-07-922-723A-53	Sequence 53, Appl
578	10.4	54.7	27	3	US-08-483-511-72	Sequence 72, Appl	651	10.2	53.7	20	2	US-07-799-828C-53	Sequence 53, Appl
579	10.4	54.7	27	3	US-09-403-066A-8	Sequence 8, Appl	652	10.2	53.7	20	2	US-08-031-147A-9	Sequence 9, Appl
580	10.4	54.7	27	3	US-09-086-436-14	Sequence 14, Appl	653	10.2	53.7	20	2	US-08-031-147A-10	Sequence 10, Appl
581	10.4	54.7	27	3	US-09-086-436-26	Sequence 26, Appl	654	10.2	53.7	20	2	US-08-031-147A-47	Sequence 47, Appl
c 582	10.4	54.7	27	3	US-09-723-000A-11	Sequence 11, Appl	655	10.2	53.7	20	2	US-08-031-147A-51	Sequence 51, Appl
583	10.4	54.7	28	3	US-09-121-539-2	Sequence 2, Appl	656	10.2	53.7	20	2	US-08-031-143B-63	Sequence 63, Appl
584	10.4	54.7	28	3	US-09-117-860-40	Sequence 40, Appl	657	10.2	53.7	20	2	US-08-555-678-49	Sequence 49, Appl
585	10.4	54.7	28	3	US-09-304-232-381	Sequence 381, App	658	10.2	53.7	20	2	US-08-173-489C-17	Sequence 17, Appl
586	10.4	54.7	29	3	US-09-830-967-2	Sequence 2, Appl	659	10.2	53.7	20	2	US-07-952-277A-53	Sequence 53, Appl
587	10.4	54.7	29	10	5212866-68	Patent No. 5212866	c 660	10.2	53.7	20	2	US-08-529-878B-23	Sequence 23, Appl
c 588	10.2	53.7	15	2	US-08-291-932A-378	Sequence 378, App	661	10.2	53.7	20	2	US-08-403-888A-125	Sequence 125, App
589	10.2	53.7	15	2	US-08-856-141-20	Sequence 20, Appl	662	10.2	53.7	20	2	US-08-403-888A-126	Sequence 126, App
590	10.2	53.7	15	3	US-09-495-140-20	Sequence 20, Appl	663	10.2	53.7	20	2	US-08-403-888A-137	Sequence 137, App
591	10.2	53.7	15	3	US-10-059-877-20	Sequence 20, Appl	664	10.2	53.7	20	2	US-08-403-888A-141	Sequence 141, App
592	10.2	53.7	15	4	US-09-341-700A-140	Sequence 140, App	c 665	10.2	53.7	20	2	US-09-048-804-6	Sequence 6, Appl
593	10.2	53.7	16	2	US-08-357-598-3	Sequence 3, Appl	c 666	10.2	53.7	20	3	US-03-429-323-46	Sequence 46, Appl
c 594	10.2	53.7	16	2	US-08-856-141-22	Sequence 22, Appl	c 667	10.2	53.7	20	3	US-08-765-340-30	Sequence 30, Appl
c 595	10.2	53.7	16	3	US-09-003-289-3	Sequence 3, Appl	668	10.2	53.7	20	3	US-09-313-932-275	Sequence 275, App
596	10.2	53.7	16	3	US-08-856-141-22	Sequence 22, Appl	c 669	10.2	53.7	20	3	US-09-662-249A-44	Sequence 44, Appl
597	10.2	53.7	16	3	US-09-479-524-6	Sequence 6, Appl	670	10.2	53.7	20	3	US-09-393-529-16	Sequence 16, Appl
598	10.2	53.7	16	3	US-09-495-140-22	Sequence 22, Appl	671	10.2	53.7	20	3	US-03-422-978-5435	Sequence 5435, Ap
599	10.2	53.7	16	3	US-10-059-877-22	Sequence 22, Appl	672	10.2	53.7	20	3	US-09-422-978-5858	Sequence 5858, Ap
c 600	10.2	53.7	16	7	PCR-US995-16435-3	Sequence 3, Appl	673	10.2	53.7	20	3	US-09-422-978-5972	Sequence 5972, Ap
c 601	10.2	53.7	17	2	US-08-173-489C-8	Sequence 8, Appl	674	10.2	53.7	20	3	US-09-422-978-7145	Sequence 7145, Ap
c 602	10.2	53.7	17	2	US-08-173-489C-92	Sequence 92, Appl	c 675	10.2	53.7	20	3	US-09-432-978-10500	Sequence 10500, A
c 603	10.2	53.7	17	3	US-08-998-099-47	Sequence 47, Appl	676	10.2	53.7	20	3	US-09-198-452A-4432	Sequence 4432, Ap
c 604	10.2	53.7	17	3	US-08-584-040-5477	Sequence 5477, Ap	c 677	10.2	53.7	20	3	US-09-198-452A-6147	Sequence 6147, Ap
605	10.2	53.7	17	3	US-09-495-140-26	Sequence 26, Appl	c 678	10.2	53.7	20	3	US-09-198-452A-6561	Sequence 6561, Ap
c 606	10.2	53.7	17	3	US-09-474-432B-821	Sequence 821, App	c 679	10.2	53.7	20	3	US-09-486-147-29	Sequence 29, Appl
c 607	10.2	53.7	17	3	US-09-474-432B-839	Sequence 839, App	680	10.2	53.7	20	3	US-09-486-147-29	Sequence 29, Appl

681	10.2	53.7	20	3	US-09-232-785-215	Sequence 215, App	754	10.2	53.7	24	3	US-10-012-231A-13	Sequence 13, Appl
c 682	10.2	53.7	20	3	US-09-866-5708-38	Sequence 38, Appl	755	10.2	53.7	24	3	US-10-015-368A-13	Sequence 13, Appl
683	10.2	53.7	20	3	US-09-863-049B-18	Sequence 18, Appl	756	10.2	53.7	24	3	US-10-006-768A-13	Sequence 13, Appl
c 684	10.2	53.7	20	3	US-09-263-446B-53	Sequence 53, Appl	757	10.2	53.7	24	3	US-10-015-671A-13	Sequence 13, Appl
685	10.2	53.7	20	7	PCT-US94-02471-9	Sequence 9, Appl	758	10.2	53.7	24	3	US-10-015-393A-13	Sequence 13, Appl
686	10.2	53.7	20	7	PCT-US94-02471-10	Sequence 10, Appl	759	10.2	53.7	24	3	US-10-011-833A-13	Sequence 13, Appl
687	10.2	53.7	20	7	PCT-US94-02471-47	Sequence 47, Appl	760	10.2	53.7	24	3	US-10-006-041A-13	Sequence 13, Appl
688	10.2	53.7	20	7	PCT-US94-02471-51	Sequence 51, Appl	761	10.2	53.7	24	3	US-10-012-064A-13	Sequence 13, Appl
689	10.2	53.7	20	7	PCT-US94-02891-63	Sequence 63, Appl	762	10.2	53.7	24	4	US-10-015-392A-13	Sequence 13, Appl
690	10.2	53.7	20	10	5352575-12	Patent No. 5352575	763	10.2	53.7	24	5	US-10-011-795B-13	Sequence 13, Appl
691	10.2	53.7	21	2	US-08-271-946A-8	Sequence 8, Appl	764	10.2	53.7	24	5	US-10-015-386A-13	Sequence 13, Appl
692	10.2	53.7	21	2	US-08-271-942A-8	Sequence 8, Appl	765	10.2	53.7	24	5	US-10-012-121A-13	Sequence 13, Appl
693	10.2	53.7	21	2	US-08-319-836B-25	Sequence 25, Appl	766	10.2	53.7	24	5	US-10-006-485A-13	Sequence 13, Appl
694	10.2	53.7	21	2	US-08-635-309-25	Sequence 25, Appl	767	10.2	53.7	24	5	US-10-006-746A-13	Sequence 13, Appl
695	10.2	53.7	21	2	US-08-505-509-11	Sequence 11, Appl	768	10.2	53.7	24	5	US-10-012-752A-13	Sequence 13, Appl
696	10.2	53.7	21	2	US-08-580-038-56	Sequence 56, Appl	769	10.2	53.7	24	5	US-10-017-253A-13	Sequence 13, Appl
697	10.2	53.7	21	2	US-08-491-690A-11	Sequence 11, Appl	770	10.2	53.7	24	5	US-10-015-715A-13	Sequence 13, Appl
698	10.2	53.7	21	2	US-08-845-998-12	Sequence 12, Appl	771	10.2	53.7	24	5	US-10-015-715A-13	Sequence 13, Appl
699	10.2	53.7	21	2	US-08-529-878B-4	Sequence 4, Appl	772	10.2	53.7	24	5	US-10-007-236A-13	Sequence 13, Appl
700	10.2	53.7	21	2	US-08-529-878B-45	Sequence 45, Appl	773	10.2	53.7	24	7	PCT-US95-12608-22	Sequence 22, Appl
701	10.2	53.7	21	3	US-08-773-916A-8	Sequence 8, Appl	774	10.2	53.7	24	10	5245022-9	Patent No. 5245022
c 702	10.2	53.7	21	3	US-09-009-913-74	Sequence 74, Appl	775	10.2	53.7	25	2	US-08-324-465-7	Sequence 7, Appl
703	10.2	53.7	21	3	US-09-206-537-12	Sequence 12, Appl	776	10.2	53.7	25	2	US-08-401-512-28	Sequence 28, Appl
704	10.2	53.7	21	3	US-08-750-232-8	Sequence 8, Appl	777	10.2	53.7	25	2	US-08-641-627A-17	Sequence 17, Appl
705	10.2	53.7	21	3	US-09-430-854-12	Sequence 12, Appl	778	10.2	53.7	25	2	US-08-641-627A-18	Sequence 18, Appl
c 706	10.2	53.7	21	3	US-08-949-344C-20	Sequence 20, Appl	779	10.2	53.7	25	2	US-08-641-627A-19	Sequence 19, Appl
c 707	10.2	53.7	21	3	US-09-553-690-17	Sequence 17, Appl	780	10.2	53.7	25	2	US-08-465-981-7	Sequence 7, Appl
708	10.2	53.7	21	3	US-09-119-507B-55	Sequence 55, Appl	c 781	10.2	53.7	25	3	US-08-737-607-31	Sequence 31, Appl
c 709	10.2	53.7	21	3	US-09-380-836-90	Sequence 90, Appl	782	10.2	53.7	25	3	US-09-226-012-16	Sequence 16, Appl
710	10.2	53.7	21	3	US-08-897-556A-55	Sequence 55, Appl	783	10.2	53.7	25	3	US-08-776-971-78	Sequence 78, Appl
711	10.2	53.7	21	7	PCT-US95-08604-8	Sequence 8, Appl	784	10.2	53.7	25	3	US-09-866-108A-3824	Sequence 3824, Ap
712	10.2	53.7	21	3	US-09-547-693-55	Sequence 55, Appl	785	10.2	53.7	25	3	US-09-866-108A-3825	Sequence 3825, Ap
c 713	10.2	53.7	21	3	US-09-657-472-1093	Sequence 1093, Ap	786	10.2	53.7	25	3	US-09-866-108A-3826	Sequence 3826, Ap
c 714	10.2	53.7	21	3	US-09-657-472-1956	Sequence 1956, Ap	787	10.2	53.7	25	3	US-09-866-108A-3827	Sequence 3827, Ap
715	10.2	53.7	21	4	US-09-684-061-10	Sequence 10, Appl	788	10.2	53.7	25	3	US-09-866-108A-3828	Sequence 3828, Ap
716	10.2	53.7	21	7	PCT-US95-08606-8	Sequence 8, Appl	789	10.2	53.7	25	3	US-09-866-108A-3829	Sequence 3829, Ap
717	10.2	53.7	21	7	PCT-US95-08606-8	Sequence 8, Appl	790	10.2	53.7	25	3	US-09-866-108A-3830	Sequence 3830, Ap
718	10.2	53.7	21	7	PCT-US95-13142-25	Sequence 25, Appl	791	10.2	53.7	25	3	US-09-866-108A-3831	Sequence 3831, Ap
719	10.2	53.7	22	3	US-08-435-350-81	Sequence 81, Appl	792	10.2	53.7	25	3	US-09-866-108A-3832	Sequence 3832, Ap
c 720	10.2	53.7	22	3	US-09-043-149-7	Sequence 7, Appl	793	10.2	53.7	25	3	US-09-866-108A-3833	Sequence 3833, Ap
c 721	10.2	53.7	23	3	US-09-061-768A-24	Sequence 24, Appl	794	10.2	53.7	25	3	US-09-866-108A-3834	Sequence 3834, Ap
c 722	10.2	53.7	23	3	US-09-537-357-37	Sequence 37, Appl	c 795	10.2	53.7	25	3	US-09-576-290-78	Sequence 78, Appl
c 723	10.2	53.7	23	3	US-09-764-246-24	Sequence 24, Appl	c 796	10.2	53.7	25	3	US-09-396-196G-9051	Sequence 9051, Ap
724	10.2	53.7	23	3	US-09-999-833A-165	Sequence 165, App	c 797	10.2	53.7	25	3	US-09-396-196G-24441	Sequence 24441, A
725	10.2	53.7	23	3	US-10-020-445A-165	Sequence 165, App	c 798	10.2	53.7	25	3	US-09-396-196G-24442	Sequence 24442, A
726	10.2	53.7	23	4	US-09-978-189-165	Sequence 165, App	c 799	10.2	53.7	25	3	US-09-396-196G-50205	Sequence 50205, A
727	10.2	53.7	23	5	US-10-017-085A-165	Sequence 165, App	c 800	10.2	53.7	25	3	US-09-396-196G-50205	Sequence 50205, A
728	10.2	53.7	23	5	US-10-145-129A-165	Sequence 165, App	c 801	10.2	53.7	25	3	US-09-396-196G-67755	Sequence 67755, A
729	10.2	53.7	23	5	US-10-013-929A-165	Sequence 165, App	c 802	10.2	53.7	25	3	US-09-396-196G-73046	Sequence 73046, A
730	10.2	53.7	23	5	US-10-013-917A-165	Sequence 165, App	c 803	10.2	53.7	25	3	US-09-396-196G-77918	Sequence 77918, A
731	10.2	53.7	24	2	US-08-466-033-222	Sequence 222, App	c 804	10.2	53.7	25	3	US-09-396-196G-80769	Sequence 80769, A
732	10.2	53.7	24	2	US-08-444-733-222	Sequence 222, App	c 805	10.2	53.7	25	3	US-09-396-196G-80943	Sequence 80943, A
733	10.2	53.7	24	2	US-08-464-134-222	Sequence 22, App	c 806	10.2	53.7	25	3	US-09-396-196G-87940	Sequence 87940, A
734	10.2	53.7	24	2	US-08-477-890-1	Sequence 1, Appl	c 807	10.2	53.7	25	3	US-09-396-196G-87941	Sequence 87941, A
735	10.2	53.7	24	2	US-08-461-361-222	Sequence 222, App	c 808	10.2	53.7	25	3	US-09-396-196G-103041	Sequence 103041, A
736	10.2	53.7	24	2	US-08-485-910-222	Sequence 222, App	c 809	10.2	53.7	25	3	US-09-396-196G-114702	Sequence 114702, A
737	10.2	53.7	24	2	US-08-467-034A-1	Sequence 1, Appl	c 810	10.2	53.7	25	3	US-09-396-196G-119048	Sequence 119048, A
738	10.2	53.7	24	3	US-09-176-862-15	Sequence 15, Appl	c 811	10.2	53.7	25	3	US-09-396-196G-119048	Sequence 119048, A
739	10.2	53.7	24	3	US-09-132-849-2	Sequence 2, Appl	c 812	10.2	53.7	25	3	US-09-396-196G-121128	Sequence 121128, A
740	10.2	53.7	24	3	US-09-132-849-2	Sequence 22, Appl	c 813	10.2	53.7	25	3	US-09-396-196G-121128	Sequence 121128, A
741	10.2	53.7	24	3	US-09-327-229-22	Sequence 22, Appl	c 814	10.2	53.7	25	3	US-10-232-459-6	Sequence 6, Appl
742	10.2	53.7	24	3	US-08-468-646A-1	Sequence 1, Appl	815	10.2	53.7	26	7	PCT-US93-11915-7	Sequence 7, Appl
743	10.2	53.7	24	3	US-08-818-082-4	Sequence 4, Appl	816	10.2	53.7	26	2	US-08-770-565-25	Sequence 25, Appl
744	10.2	53.7	24	3	US-09-115-387-2	Sequence 2, Appl	817	10.2	53.7	26	2	US-08-887-798-22	Sequence 22, Appl
c 745	10.2	53.7	24	3	US-09-369-912-6	Sequence 6, Appl	818	10.2	53.7	26	3	US-08-765-340A-4	Sequence 4, Appl
746	10.2	53.7	24	3	US-08-455-014B-1	Sequence 1, Appl	c 819	10.2	53.7	26	3	US-09-720-435A-486	Sequence 486, App
747	10.2	53.7	24	3	US-08-471-645A-1	Sequence 1, Appl	820	10.2	53.7	26	3	US-09-998-976-6	Sequence 6, Appl
748	10.2	53.7	24	3	US-09-692-056-4	Sequence 4, Appl	c 821	10.2	53.7	27	2	US-08-647-584-20	Sequence 20, Appl
749	10.2	53.7	24	3	US-10-144-669-2	Sequence 2, Appl	822	10.2	53.7	27	2	US-08-609-443B-27	Sequence 27, Appl
750	10.2	53.7	24	3	US-09-216-430C-30	Sequence 30, Appl	823	10.2	53.7	27	2	US-08-467-034A-6	Sequence 6, Appl
751	10.2	53.7	24	3	US-09-439-429-15	Sequence 15, Appl	824	10.2	53.7	27	3	US-08-468-646A-6	Sequence 6, Appl
752	10.2	53.7	24	3	US-09-001-039B-1	Sequence 1, Appl	825	10.2	53.7	27	3	US-08-851-896-27	Sequence 27, Appl
753	10.2	53.7	24	3	US-09-735-271-1822	Sequence 1822, Ap	826	10.2	53.7	27	3	US-08-455-014B-6	Sequence 6, Appl

827	10.2	53.7	27	3	US-08-471-645A-6	Sequence 6, Appli	900	10	52.6	19	5	US-09-543-679A-1515	Sequence 1515, Ap
c 828	10.2	53.7	27	3	US-09-428-082B-383	Sequence 383, App	c 901	10	52.6	20	2	US-08-149-105-6	Sequence 6, Appli
829	10.2	53.7	27	3	US-09-795-061-23	Sequence 23, Appl	c 902	10	52.6	20	2	US-08-317-847-6	Sequence 6, Appli
830	10.2	53.7	27	3	US-09-001-039B-9	Sequence 9, Appli	c 903	10	52.6	20	3	US-09-166-186-9	Sequence 9, Appli
c 831	10.2	53.7	27	4	US-09-856-725-6	Sequence 6, Appli	c 904	10	52.6	20	3	US-09-092-077-34	Sequence 34, Appli
c 832	10.2	53.7	28	2	US-08-362-670B-24	Sequence 24, Appl	c 905	10	52.6	20	3	US-09-313-932-9	Sequence 9, Appli
c 833	10.2	53.7	28	2	US-08-647-584-21	Sequence 21, Appl	c 906	10	52.6	20	3	US-09-313-932-430	Sequence 430, App
c 834	10.2	53.7	28	2	US-08-477-890-2	Sequence 2, Appli	c 907	10	52.6	20	3	US-09-428-583-13	Sequence 13, Appl
c 835	10.2	53.7	28	3	US-08-467-034A-2	Sequence 2, Appli	c 908	10	52.6	20	3	US-09-309-317-21	Sequence 21, Appl
c 836	10.2	53.7	28	3	US-08-333-576C-24	Sequence 24, Appl	c 909	10	52.6	20	3	US-09-404-056-4	Sequence 4, Appli
837	10.2	53.7	28	3	US-08-846-020A-2	Sequence 2, Appli	c 910	10	52.6	20	3	US-09-457-046B-38	Sequence 38, Appl
c 838	10.2	53.7	28	3	US-08-468-646A-2	Sequence 2, Appli	c 911	10	52.6	20	3	US-09-422-978-7954	Sequence 7954, Ap
c 839	10.2	53.7	28	3	US-08-808-324-24	Sequence 24, Appl	c 912	10	52.6	20	3	US-09-198-452A-2758	Sequence 2758, Ap
840	10.2	53.7	28	3	US-08-891-292A-94	Sequence 94, Appl	c 913	10	52.6	20	3	US-09-198-452A-4303	Sequence 4303, Ap
841	10.2	53.7	28	3	US-09-617-871-2	Sequence 2, Appli	c 914	10	52.6	20	3	US-09-940-244-187	Sequence 187, App
c 842	10.2	53.7	28	3	US-08-455-014B-2	Sequence 2, Appli	c 915	10	52.6	20	3	US-09-940-244-188	Sequence 188, App
c 843	10.2	53.7	28	3	US-08-471-645A-2	Sequence 2, Appli	c 916	10	52.6	20	3	US-09-940-244-189	Sequence 189, App
c 844	10.2	53.7	28	3	US-09-927-737C-94	Sequence 94, Appl	c 917	10	52.6	20	3	US-09-893-440-13	Sequence 13, Appl
c 845	10.2	53.7	28	3	US-09-732-615-24	Sequence 24, Appl	c 918	10	52.6	20	3	US-09-713-737-7	Sequence 7, Appli
c 846	10.2	53.7	28	3	US-09-945-182-24	Sequence 24, Appl	c 919	10	52.6	20	3	US-09-672-126B-127	Sequence 127, App
c 847	10.2	53.7	28	3	US-09-945-182-24	Sequence 24, Appl	c 920	10	52.6	20	3	US-09-672-126B-128	Sequence 128, App
c 848	10.2	53.7	28	3	US-10-273-051-24	Sequence 24, Appl	c 921	10	52.6	20	4	US-09-912-724-37	Sequence 37, Appl
c 849	10.2	53.7	28	3	US-09-001-039B-2	Sequence 2, Appli	c 922	10	52.6	20	5	US-09-670-105-34	Sequence 34, Appl
c 850	10.2	53.7	28	4	US-10-779-635-24	Sequence 24, Appl	c 923	10	52.6	20	5	US-09-543-679A-1278	Sequence 1278, Ap
c 851	10.2	53.7	29	2	US-08-647-584-45	Sequence 45, Appl	c 924	10	52.6	21	2	US-08-256-426B-282	Sequence 282, App
c 852	10.2	53.7	29	3	US-09-434-840-44	Sequence 44, Appl	c 925	10	52.6	21	2	US-08-437-607A-12	Sequence 12, Appl
853	10.2	53.7	30	2	US-08-802-547-14	Sequence 14, Appl	c 926	10	52.6	21	3	US-08-757-024-2	Sequence 2, Appli
854	10.2	53.7	30	2	US-08-678-039A-34	Sequence 34, Appl	c 927	10	52.6	21	3	US-08-472-527-2	Sequence 2, Appli
855	10.2	53.7	30	2	US-08-859-998-136	Sequence 136, App	c 928	10	52.6	21	3	US-09-109-663-59	Sequence 59, Appli
856	10.2	53.7	30	3	US-09-225-928-136	Sequence 136, App	c 929	10	52.6	21	3	US-09-245-159-7	Sequence 7, Appli
857	10.2	53.7	30	3	US-09-225-201B-136	Sequence 136, App	c 930	10	52.6	21	3	US-09-380-836-58	Sequence 58, Appl
c 858	10.2	53.7	30	3	US-09-119-507B-54	Sequence 54, Appl	c 931	10	52.6	21	3	US-09-382-552-168	Sequence 168, App
c 859	10.2	53.7	30	3	US-08-897-556A-54	Sequence 54, Appl	c 932	10	52.6	21	3	US-09-940-244-174	Sequence 174, App
c 860	10.2	53.7	30	3	US-09-732-615-22	Sequence 22, Appl	c 933	10	52.6	21	3	US-09-940-244-181	Sequence 181, App
c 861	10.2	53.7	30	3	US-09-547-693-54	Sequence 54, Appl	c 934	10	52.6	21	3	US-09-940-244-186	Sequence 186, App
c 862	10.2	53.7	30	3	US-10-273-051-22	Sequence 22, Appl	c 935	10	52.6	21	3	US-09-657-472-1763	Sequence 1763, Ap
863	10.2	53.7	30	3	US-09-780-929-114	Sequence 114, App	c 936	10	52.6	21	3	US-10-071-411A-4	Sequence 4, Appli
c 864	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 937	10	52.6	21	3	US-09-085-849-7	Sequence 7, Appli
c 865	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 938	10	52.6	21	3	US-09-093-972C-2	Sequence 2, Appli
c 866	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 939	10	52.6	21	3	US-09-085-849-7	Sequence 7, Appli
c 867	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 940	10	52.6	21	3	US-09-875-453B-96	Sequence 96, Appl
c 868	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 941	10	52.6	21	3	US-09-381-212-186	Sequence 186, App
c 869	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 942	10	52.6	21	3	US-09-381-212-187	Sequence 187, App
c 870	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 943	10	52.6	21	3	US-09-381-212-188	Sequence 188, App
c 871	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 944	10	52.6	21	3	US-09-381-212-189	Sequence 189, App
c 872	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 945	10	52.6	21	3	US-09-713-601A-186	Sequence 186, App
c 873	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 946	10	52.6	21	3	US-09-713-601A-187	Sequence 187, App
c 874	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 947	10	52.6	21	3	US-09-713-601A-188	Sequence 188, App
c 875	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 948	10	52.6	21	3	US-09-713-601A-189	Sequence 189, App
c 876	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 949	10	52.6	21	3	US-09-543-679A-2	Sequence 2, Appli
c 877	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 950	10	52.6	21	3	US-08-660-645A-37	Sequence 37, Appl
c 878	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 951	10	52.6	21	3	US-09-298-718-37	Sequence 37, Appl
c 879	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 952	10	52.6	21	3	US-09-546-969-37	Sequence 37, Appl
c 880	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 953	10	52.6	21	3	US-08-980-832-16	Sequence 16, Appl
c 881	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 954	10	52.6	21	3	US-09-547-267-37	Sequence 37, Appl
c 882	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 955	10	52.6	21	3	US-09-920-923B-16	Sequence 16, Appl
c 883	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 956	10	52.6	21	3	US-09-940-244-182	Sequence 182, App
c 884	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 957	10	52.6	21	3	US-09-381-212-174	Sequence 174, App
c 885	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 958	10	52.6	21	3	US-09-381-212-181	Sequence 181, App
c 886	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 959	10	52.6	21	3	US-09-713-601A-174	Sequence 174, App
c 887	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 960	10	52.6	21	3	US-08-577-601A-181	Sequence 181, App
c 888	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 961	10	52.6	21	3	US-08-577-601A-182	Sequence 182, App
c 889	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 962	10	52.6	21	3	US-08-577-601A-183	Sequence 183, App
c 890	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 963	10	52.6	21	3	US-08-577-601A-184	Sequence 184, App
c 891	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 964	10	52.6	21	3	US-08-577-601A-185	Sequence 185, App
c 892	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 965	10	52.6	21	3	US-08-577-601A-186	Sequence 186, App
c 893	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 966	10	52.6	21	3	US-08-577-601A-187	Sequence 187, App
c 894	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 967	10	52.6	21	3	US-08-577-601A-188	Sequence 188, App
c 895	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 968	10	52.6	21	3	US-08-577-601A-189	Sequence 189, App
c 896	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 969	10	52.6	21	3	US-08-577-601A-190	Sequence 190, App
c 897	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 970	10	52.6	21	3	US-08-577-601A-191	Sequence 191, App
c 898	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 971	10	52.6	21	3	US-08-577-601A-192	Sequence 192, App
c 899	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 972	10	52.6	21	3	US-08-577-601A-193	Sequence 193, App

C 973 10 52.6 24 2 US-08-592-820-13 Sequence 13, Appl
C 974 10 52.6 24 2 US-08-858-767-1 Sequence 1, Appl
C 975 10 52.6 24 2 US-08-858-767-3 Sequence 3, Appl
C 976 10 52.6 24 2 US-08-863-028-1 Sequence 1, Appl
C 977 10 52.6 24 2 US-08-863-028-3 Sequence 3, Appl
C 978 10 52.6 24 2 US-08-547-214-1 Sequence 1, Appl
C 979 10 52.6 24 2 US-08-547-214-15 Sequence 15, Appl
C 980 10 52.6 24 2 US-08-761-277A-59 Sequence 59, Appl
C 981 10 52.6 24 2 US-08-663-823B-1 Sequence 1, Appl
C 982 10 52.6 24 2 US-08-663-823B-15 Sequence 15, Appl
C 983 10 52.6 24 2 US-08-663-823B-60 Sequence 60, Appl
C 984 10 52.6 24 2 US-08-663-823B-62 Sequence 62, Appl
C 985 10 52.6 24 2 US-08-993-118-11 Sequence 11, Appl
C 986 10 52.6 24 3 US-08-748-130-23 Sequence 23, Appl
C 987 10 52.6 24 3 US-08-392-794A-13 Sequence 13, Appl
C 988 10 52.6 24 3 US-08-845-528C-11 Sequence 11, Appl
C 989 10 52.6 24 3 US-08-874-825-27 Sequence 27, Appl
C 990 10 52.6 24 3 US-08-874-825-29 Sequence 29, Appl
C 991 10 52.6 24 3 US-08-874-825-31 Sequence 31, Appl
C 992 10 52.6 24 3 US-08-874-825-33 Sequence 33, Appl
C 993 10 52.6 24 3 US-08-874-825-53 Sequence 53, Appl
C 994 10 52.6 24 3 US-08-874-825-67 Sequence 67, Appl
C 995 10 52.6 24 3 US-08-874-825-107 Sequence 107, App
C 996 10 52.6 24 3 US-08-874-825-109 Sequence 109, App
C 997 10 52.6 24 3 US-08-663-824-27 Sequence 27, Appl
C 998 10 52.6 24 3 US-08-663-824-29 Sequence 29, Appl
C 999 10 52.6 24 3 US-08-663-824-31 Sequence 31, Appl
C1000 10 52.6 24 3 US-08-663-824-33 Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-914-961-8/c
; Sequence 8, Application US/08914961
; Patent No. 6018042
; GENERAL INFORMATION:
; APPLICANT: Mett, Helmut
; APPLICANT: Hanert, Robert
; APPLICANT: Dean, Nicholas Mark
; TITLE OF INVENTION: Antitumor Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GRIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914, 961
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/287,753
; FILING DATE: 09-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprull, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 4-20047/P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; POSITION IN GENOME:
; MAP POSITION: 1046
; UNITS: bp
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..20
; OTHER INFORMATION: /note= "All nucleotides are of the
; OTHER INFORMATION: phosphorothioate type"
US-08-914-961-8
Query Match 72.6%; Score 13.8; DB 3; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 AGAAGGGGTGGTGCT 19
Db 19 AGAAGGTGGTGATGCT 3
RESULT 2
US-10-085-612A-23/c
; Sequence 23, Application US/10085612A
; Patent No. 6929912
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Colvin, Oliver
; APPLICANT: Vredenburgh, James
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: METHODS FOR EVALUATING THE ABILITY TO METABOLIZE PHARMACEUTICALS
; FILE REFERENCE: DNA-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-612A-23
Query Match 70.5%; Score 13.4; DB 3; Length 22;
Best Local Similarity 93.3%; Pred. No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGAGAGGGGTGGG 15
Db 22 GGAGAGGAGGTGGG 8
RESULT 3
US-09-422-978-9827/c
; Sequence 9827, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/067,626
APPLICATION NUMBER: US/09/067,626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,688
FILING DATE: 06-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/491
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-067-626-12

Query Match          69.5%;   Score 13.2;   DB 3;   Length 25;
Best Local Similarity 83.3%;   Pred. No. 6.7e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      1  GGAGAAAGGGGGTGGGTGC 18
      ||| ||| ||| ||| ||| |||
Db      1  GGGGATGGCGTGGGTGC 18

RESULT 6
US-08-173-489C-359/c
Sequence 359, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959

```

```
; INFORMATION FOR SEQ ID NO: 359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: p53 gene, nucleotides 1427-1453
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Harlow, E, Williamson, N M, Ralston, R,
;          Helfman, D M, Adams T E.
; TITLE: Molecular cloning and in
; TITLE: vitro expression of a cDNA for human cellular
; TITLE: tumor antigen p53
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; PAGES: 1601-1610
; DATE: 1985
; RELEVANT RESIDUES IN SEQ ID NO: 359 :FROM 1 TO 27
US-08-173-489C-359

Query Match          67.4%; Score 12.8; DB 2; Length 27;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GAGAGGGGGTGGGTG 17
Db      17 GAGATGGGGTGGGAG 2

RESULT 7
US-08-943-731-424
; Sequence 424, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLR
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 424:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-424

Query Match          66.3%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGGGTGCT 19
Db      3 GGAAATGAGGTGGGTGCT 21

RESULT 8
US-09-282-146-4/c
; Sequence 4, Application US/09282146A
; Patent No. 6303847
; GENERAL INFORMATION:
; APPLICANT: KAWAOKA, Akiyoshi
; APPLICANT: EBINUMA, Hiroyasu
; TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID
; TITLE OF INVENTION: BIOSYNTHESIS PATHWAY
; FILE REFERENCE: 4859-0027-0
; CURRENT APPLICATION NUMBER: US/09/282,146A
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: JP 10-125171
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-282-146-4

Query Match          65.3%; Score 12.4; DB 3; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GAAGGGGGTGGGTG 17
Db      17 GAAGGGGGTGGTG 4

RESULT 9
US-09-205-921-33
; Sequence 33, Application US/09205921A
; Patent No. 6008048
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: ex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF EGR-1 EXPRESSION
; FILE REFERENCE: RTS-0028
; CURRENT APPLICATION NUMBER: US/09/205,921A
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
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```
; SEQ ID NO 33
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-203-921-33

Query Match      65.3%; Score 12.4; DB 3; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGG 14
Db 5 GGAGAAGGGGGTGG 18

RESULT 10
US-09-472-246
; Sequence 246, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2835.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-246

Query Match      65.3%; Score 12.4; DB 3; Length 21;
Best Local Similarity 81.2%; Pred. No. 1.5e+04;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAAGGGGGTGGTGTCT 19
Db 3 GAAGAGGGGGGTACT 18

RESULT 11
US-08-927-219-64/c
; Sequence 64, Application US/08927219
; Patent No. 6187533
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamagata, Kazuya
; APPLICANT: Oda, Naohisa
; APPLICANT: Katsaki, Pamela J.
; APPLICANT: Furuta, Hiroto
; APPLICANT: Horikawa, Yukio
; APPLICANT: Menzel, Stephen
; TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
; TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
; TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-4ALPHA
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

; SEQ ID NO 33
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,219
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,679
; FILING DATE: 30-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,056
; FILING DATE: 02-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,719
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-927-219-64

Query Match      65.3%; Score 12.4; DB 3; Length 22;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGG 14
Db 14 GGAGTAGGGGGTGG 1

RESULT 12
US-09-716-964B-191/c
; Sequence 191, Application US/09716964B
; Patent No. 6897053
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; FILE REFERENCE: 2221/1030
; CURRENT APPLICATION NUMBER: US/09/716,964B
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 191
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; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-716-964B-191

Query Match      65.3%; Score 12.4; DB 3; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGG 14
Db      19 GGAGAGGGTGGTGG 6

RESULT 13
US-08-504-511A-6/c
; Sequence 6, Application US/08504511A
; Patent No. 5561224
; GENERAL INFORMATION:
; APPLICANT: Rosenfeld, M. G.
; APPLICANT: Andersen, B.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
; TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/504,511A
; FILING DATE: 20-JUL-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; IMMEDIATE SOURCE:
; CLONE: Skn-11 POU
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..30
US-08-504-511A-6

Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGG 14
Db      24 GGAGAGGAGGGTGG 11
```

```
RESULT 14
US-09-119-507B-10/c
; Sequence 10, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-10

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGG 14
Db      29 GGAGATGGGGTGG 16

RESULT 15
US-09-119-507B-38/c
; Sequence 38, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-38

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGG 14
Db      29 GGAGATGGGGTGG 16

RESULT 16
US-09-119-507B-39
; Sequence 39, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 30
; TYPE: DNA
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```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-39

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGG 14
    ||||| |||||
Db 11 GGAGATGGGGTGG 24

RESULT 17
US-08-897-556A-10/c
; Sequence 10, Application US/08897556A
; Patent No. 6570062
; GENERAL INFORMATION:
; APPLICANT: KIELSZEWSKI, MARCIA J.
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897.556A
; FILING DATE: 21-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02908
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-897-556A-10

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGG 14
    ||||| |||||
Db 29 GGAGATGGGGTGG 16

RESULT 18
US-08-897-556A-38/c
; Sequence 38, Application US/08897556A
; Patent No. 6570062
; GENERAL INFORMATION:
; APPLICANT: KIELSZEWSKI, MARCIA J.
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
```

```
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897.556A
; FILING DATE: 21-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02908
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-897-556A-38

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGG 14
    ||||| |||||
Db 29 GGAGATGGGGTGG 16

RESULT 19
US-08-897-556A-39
; Sequence 39, Application US/08897556A
; Patent No. 6570062
; GENERAL INFORMATION:
; APPLICANT: KIELSZEWSKI, MARCIA J.
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897.556A
; FILING DATE: 21-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02908
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 US-08-897-556A-39

Query Match 65.3%; Score 12.4; DB 3; Length 30;
 Best Local Similarity 92.9%; Pred. No. 1.5e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGG 14
 ||||| |||||
 Db 11 GGAGATGGGGTGG 24

RESULT 20
 US-09-547-693-10/c
 Sequence 10, Application US/09547693
 Patent No. 6639050
 GENERAL INFORMATION:
 APPLICANT: Kieliszewski, Marcia
 TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
 TITLE OF INVENTION: Glycoproteins
 FILE REFERENCE: OHU-04089
 CURRENT APPLICATION NUMBER: US/09/547,693
 CURRENT FILING DATE: 2000-04-12
 NUMBER OF SEQ ID NOS: 236
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 10
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Artificial/Unknown
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Synthetic
 US-09-547-693-10

Query Match 65.3%; Score 12.4; DB 3; Length 30;
 Best Local Similarity 92.9%; Pred. No. 1.5e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGG 14
 ||||| |||||
 Db 29 GGAGATGGGGTGG 16

RESULT 21
 US-09-547-693-38/c
 Sequence 38, Application US/09547693
 Patent No. 6639050
 GENERAL INFORMATION:
 APPLICANT: Kieliszewski, Marcia
 TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
 TITLE OF INVENTION: Glycoproteins
 FILE REFERENCE: OHU-04089
 CURRENT APPLICATION NUMBER: US/09/547,693
 CURRENT FILING DATE: 2000-04-12
 NUMBER OF SEQ ID NOS: 236
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 38
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Artificial/Unknown
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Synthetic
 US-09-547-693-38

Query Match 65.3%; Score 12.4; DB 3; Length 30;
 Best Local Similarity 92.9%; Pred. No. 1.5e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GGAGAGGGGGTGG 14
 ||||| |||||
 Db 29 GGAGATGGGGTGG 16

RESULT 22
 US-09-547-693-39
 Sequence 39, Application US/09547693
 Patent No. 6639050
 GENERAL INFORMATION:
 APPLICANT: Kieliszewski, Marcia
 TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
 TITLE OF INVENTION: Glycoproteins
 FILE REFERENCE: OHU-04089
 CURRENT APPLICATION NUMBER: US/09/547,693
 CURRENT FILING DATE: 2000-04-12
 NUMBER OF SEQ ID NOS: 236
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 39
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Artificial/Unknown
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Synthetic
 US-09-547-693-39

Query Match 65.3%; Score 12.4; DB 3; Length 30;
 Best Local Similarity 92.9%; Pred. No. 1.5e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGG 14
 ||||| |||||
 Db 11 GGAGATGGGGTGG 24

RESULT 23
 US-08-531-556-122/c
 Sequence 122, Application US/08531556
 Patent No. 5776682
 GENERAL INFORMATION:
 APPLICANT: Agoulrik, Alexander I
 APPLICANT: Kent First, Marijo
 APPLICANT: Muallem, Arlege
 TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
 TITLE OF INVENTION: BATTERY
 NUMBER OF SEQUENCES: 124
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Demitt Ross & Stevens, S.C.
 STREET: 8000 Excelsior Drive, Suite 401
 CITY: Madison
 STATE: WI
 COUNTRY: USA
 ZIP: 53717-1914
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/531,556
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Sara Charles S.
 REGISTRATION NUMBER: 30,492
 REFERENCE/DOCKET NUMBER: 34506.034CIP
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-531-556-122

Query Match 64.2%; Score 12.2; DB 2; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGGGGTGGTG 17
Db 18 GAAGAAGGGGGATGGTG 2

RESULT 24

US-08-690-734A-81/c
Sequence 81, Application US/08690734A
Patent No. 5871920

GENERAL INFORMATION:
APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
TITLE OF INVENTION: DAZ: A GENE ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,734A
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WHI94-07A
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-690-734A-81

Query Match 64.2%; Score 12.2; DB 2; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGGGGTGGTG 17
Db 18 GAAGAAGGGGGATGGTG 2

RESULT 25

US-08-742-185-81/c
Sequence 81, Application US/08742185
Patent No. 6020476

GENERAL INFORMATION:
APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-JUL-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WHI94-07A2
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-742-185-81

Query Match 64.2%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGGGGTGGTG 17
Db 18 GAAGAAGGGGGATGGTG 2

RESULT 26

US-08-448-386A-10/c
Sequence 10, Application US/08448386A
Patent No. 5840708

GENERAL INFORMATION:

APPLICANT: START Technology, Partnership
TITLE OF INVENTION: Administration of Oligonucleotides
TITLE OF INVENTION: Antisense to Dopamine Receptor mRNA for Diagnosis and
TITLE OF INVENTION: Treatment of Pathological Conditions of the Dopaminergic
TITLE OF INVENTION: Nervous System
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA

COUNTRY: USA
 ZIP: 19103-2307
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/448,386A
 FILING DATE: 14-DEC-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/991,582
 FILING DATE: 14-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: YES
 US-08-448-386A-10

Query Match 64.2%; Score 12.2; DB 2; Length 20;
 Best Local Similarity 82.4%; Pred. No. 1.8e+04;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGTG 17
 Db 17 GGAGATGGAGGTAGTG 1

RESULT 27
 US-08-816-426-10/c
 Sequence 10, Application US/08816426
 Patent No. 6025193
 GENERAL INFORMATION:
 APPLICANT: START Technology, Partnership
 TITLE OF INVENTION: Administration of Oligonucleotides
 TITLE OF INVENTION: Antisense to Dopamine Receptor mRNA for Diagnosis and
 TITLE OF INVENTION: Treatment of Pathological Conditions of the Dopaminergic
 TITLE OF INVENTION: Nervous System
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dann, Dorfman, Herrell and Skillman
 STREET: 1601 Market Street Suite 720
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-2307
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/816,426
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/448,386
 FILING DATE:
 APPLICATION NUMBER: US 07/991,582
 FILING DATE: 14-DEC-1992
 ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: YES
 US-08-816-426-10

Query Match 64.2%; Score 12.2; DB 3; Length 20;
 Best Local Similarity 82.4%; Pred. No. 1.8e+04;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGTG 17
 Db 17 GGAGATGGAGGTAGTG 1

RESULT 28
 US-08-943-731-533/c
 Sequence 533, Application US/08943731
 Patent No. 6265157
 GENERAL INFORMATION:
 APPLICANT: PROCKOP, DARWIN J.
 APPLICANT: SPOTILA, LORETTA D.
 APPLICANT: DELTAS, CONSTANTINOS D.
 APPLICANT: SEREDA, LARISA
 APPLICANT: LARSON, ANDREA W.
 APPLICANT: PACK, MICHAEL
 APPLICANT: COLIGE, ALAIN
 APPLICANT: EARLY, JAMES
 APPLICANT: KORKKO, JARMO
 APPLICANT: ALA-KOKKO, LEENA, et al.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
 TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
 NUMBER OF SEQUENCES: 666
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
 STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
 STREET: FLR.
 CITY: PHILADELPHIA
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-7086
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,731
 FILING DATE: 03-OCT-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,322
 FILING DATE: 14-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/803,628
 FILING DATE: 03-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: DOYLE LEARY Ph.D., KATHRYN
 REGISTRATION NUMBER: 36,317
 REFERENCE/DOCKET NUMBER: 9598-27
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-965-1284
 TELEFAX: 215-567-2991

```
;
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 533:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-533

Query Match          64.2%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
    ||||| ||||| ||
Db 17 GGAGATGGGGGTGTCTG 1

RESULT 29
US-08-943-731-534
; Sequence 534, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KORKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 534:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-534

Query Match          64.2%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
    ||||| ||||| ||
Db 4 GGAGATGGGGGTGTCTG 20

RESULT 30
US-09-198-452A-6511/c
; Sequence 6511, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6511
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6511

Query Match          64.2%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAAGGGGGTGGGTGC 18
    ||||| ||||| ||
Db 19 GAGAAGAGGGGTAGGAGC 3

RESULT 31
US-09-865-879-29/c
; Sequence 29, Application US/09865879
; Patent No. 6767705
; GENERAL INFORMATION:
; APPLICANT: Roninson, Igor
; APPLICANT: Dokmanovic, Milos
; APPLICANT: Chang, Bey-Dih
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION OF
; TITLE OF INVENTION: REGULATED BY RETINOIDS
; FILE REFERENCE: 99,216-H
; CURRENT APPLICATION NUMBER: US/09/865,879
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,535
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Antisense primer for P28 alpha
US-09-865-879-29

Query Match          64.2%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
    ||||| ||||| ||
```

Db 19 GAAGAAGGGGAGGATG 3

RESULT 32

PCT-US93-12161-10/c

Sequence 10, Application PC/TUS9312161

GENERAL INFORMATION:

APPLICANT: START Technology Partnership

TITLE OF INVENTION: Administration of

TITLE OF INVENTION: Oligonucleotides Antisense to Dopamine Receptor

TITLE OF INVENTION: mRNA for Diagnosis and Treatment of Pathological

TITLE OF INVENTION: Conditions of the Dopaminergic Nervous System

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and

ADDRESSEE: Skillman

STREET: 1601 Market Street, Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

SOFTWARE: #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/12161

FILING DATE: 14-DEC-1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/991,582

FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

PCT-US93-12161-10

Query Match 64.2%; Score 12.2; DB 7; Length 20;

Best Local Similarity 82.4%; Pred. No. 1.8e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGAAGGGGTGGTG 17

Db 17 GGAGATGGAGGTAGTG 1

RESULT 33

US-10-118-079-12/c

Sequence 12, Application US/10118079

Patent No. 6855688

GENERAL INFORMATION:

APPLICANT: MCKERRACHER, LISA

TITLE OF INVENTION: FUSION PROTEINS

FILE REFERENCE: 06746-004-US-03

CURRENT APPLICATION NUMBER: US/10/118,079

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: CA 2,367,636

PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: CA 2,362,004

;

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: CA 2,342,970

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn version 3.1

SEQ ID NO 12

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide used in the amplification of a sequence corresponding to amino acid 27-72 of HIV-1 Tat

US-10-118-079-12

Query Match 64.2%; Score 12.2; DB 3; Length 21;

Best Local Similarity 82.4%; Pred. No. 1.8e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGAAGGGGTGGTGCT 19

Db 17 AGAAGGTGGTGGCTGT 1

RESULT 34

US-08-330-123A-6/c

Sequence 6, Application US/08330123A

Patent No. 5583016

GENERAL INFORMATION:

APPLICANT: VILLEPONTREAU, Bryant

APPLICANT: FENG, Junli

APPLICANT: FUNK, Walter

APPLICANT: ANDREWS, William H.

TITLE OF INVENTION: HUMAN TELOMERASE

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/330,123A

FILING DATE: 27-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15389-000810

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

US-08-330-123A-6

Query Match 64.2%; Score 12.2; DB 2; Length 22;

Best Local Similarity 82.4%; Pred. No. 1.8e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGC 18
|||||
Db 18 GAGAGGGCGTAGGCG 2

RESULT 35
US-08-660-678A-28/c
; Sequence 28, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678A-28

Query Match 64.2%; Score 12.2; DB 2; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGC 18
|||||
Db 18 GAGAGGGCGTAGGCG 2

RESULT 36
US-08-485-778-8/c
; Sequence 8, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol

; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-485-778-8

Query Match 64.2%; Score 12.2; DB 2; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGC 18
|||||
Db 18 GAGAGGGCGTAGGCG 2

RESULT 37
US-08-472-802C-43/c
; Sequence 43, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-472-802C-43

Query Match 64.2%; Score 12.2; DB 2; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGC 18
|||||
DB 18 GAGAGGGGGTGGTGC 2

RESULT 38
US-09-068-109-3
Sequence 3, Application US/09068109
Patent No. 5986172
GENERAL INFORMATION:
APPLICANT: UCHIMIYA, HIROFUMI
APPLICANT: FUSHIMI, TAKAOMI
APPLICANT: KUDOU, UWE
APPLICANT: TAGAWA, MICHITO
TITLE OF INVENTION: RICE NADH-DEPENDENT REDUCTASE, GENE THEREFOR AND USE
FILE REFERENCE: 0049-0250-0 PCT
CURRENT APPLICATION NUMBER: US/09/068,109
CURRENT FILING DATE: 1998-05-05
EARLIER APPLICATION NUMBER: PCT/JP95/02641
EARLIER FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-068-109-3

Query Match 64.2%; Score 12.2; DB 2; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGTGTCT 19
|||||
DB 1 AGTACGGGGTGGTGTCT 17

RESULT 39
US-08-520-550A-8/c
Sequence 8, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-8

Query Match 64.2%; Score 12.2; DB 3; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGC 18
|||||
DB 18 GAGAGGGGGTGGTGC 2

RESULT 40
US-08-998-443-28/c
Sequence 28, Application US/08998443
Patent No. 6054575
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US/08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-998-443-28

Query Match 64.2%; Score 12.2; DB 3; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGGTGC 18
Db 18 GAGAGGGGGTGGGTGC 2

RESULT 41
US-09-580-517-6/c
Sequence 6, Application US/09580517
Patent No. 6320039
GENERAL INFORMATION:
APPLICANT: VILLEPONTAU, Bryant
FUNK, Junli
ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/580,517
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-580-517-6

Query Match 64.2%; Score 12.2; DB 3; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGGTGC 18
Db 18 GAGAGGGGGTGGGTGC 2

RESULT 42
US-09-057-351-42/c
Sequence 42, Application US/09057351
Patent No. 6548298
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-09-057-351-42

Query Match 64.2%; Score 12.2; DB 3; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGGTGC 18
|||||
Db 18 GAGAGGGCGTAGGCGC 2

RESULT 43
US-09-070-980A-2
Sequence 2, Application US/09070980A
Patent No. 6110725
GENERAL INFORMATION:
APPLICANT: DELLEY, MICHELE
APPLICANT: GERMOND, JACQUES
APPLICANT: LAPIERRE, LUCIANE
APPLICANT: MOLLET, BEAT
APPLICANT: PRIDMORE, RAYMOND
TITLE OF INVENTION: PRODUCTION OF L(+)-LACTATE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: VOGT&O'DONNELL, LLP
STREET: 707 WESTCHESTER AVENUE
CITY: WHITE PLAINES
STATE: NEW YORK
COUNTRY: USA
ZIP: 10604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,980A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 97201337.9
FILING DATE: 03-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: PLAUTZ, DAVID
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 328 00 55
TELEFAX: (914) 328 00 60
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-070-980A-2

Query Match 64.2%; Score 12.2; DB 3; Length 23;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTG 17
|||||
Db 6 GTAGAGGGCGGTGTG 22

RESULT 44
US-09-490-217-2
Sequence 2, Application US/09490217
Patent No. 6258587
GENERAL INFORMATION:
APPLICANT: DELLEY, MICHELE
APPLICANT: GERMOND, JACQUES
APPLICANT: LAPIERRE, LUCIANE
APPLICANT: MOLLET, BEAT
APPLICANT: PRIDMORE, RAYMOND
TITLE OF INVENTION: PRODUCTION OF L(+)-LACTATE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: VOGT&O'DONNELL, LLP
STREET: 707 WESTCHESTER AVENUE
CITY: WHITE PLAINES
STATE: NEW YORK
COUNTRY: USA
ZIP: 10604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,217
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,980
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PLAUTZ, DAVID
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 328 00 55
TELEFAX: (914) 328 00 60
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-490-217-2

Query Match 64.2%; Score 12.2; DB 3; Length 23;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTG 17
|||||
Db 6 GTAGAGGGCGGTGTG 22

RESULT 45
US-08-729-598-7
Sequence 7, Application US/08729598
Patent No. 6001657
GENERAL INFORMATION:
APPLICANT: Hardin, Charles C.
APPLICANT: Brown II, Bernard A.
APPLICANT: Roberts, John J.
TITLE OF INVENTION: Antibodies That Selectively Bind
TITLE OF INVENTION: Quadruplex Nucleic Acids
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sorojini J. Biswas
STREET: P.O. Box 37428
CITY: Raleigh
STATE: No. 6001657th Carolina

;; COUNTRY: USA
;; ZIP: 27627
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/729,598
;; FILING DATE: 11-OCT-1996
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Biswas, Sorojini J.
;; REGISTRATION NUMBER: 39,111
;; REFERENCE/DOCKET NUMBER: 5051-301A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919) 854-1400
;; TELEFAX: (919) 854-1401
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: DNA (genomic)
US-08-729-598-7

Query Match 64.2%; Score 12.2; DB 3; Length 24;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGGTG 17
||||| ||||| |||||
Db 7 GGAGAGGGGGGAGGGG 23

RESULT 46
US-08-547-2
; Sequence 2, Application US/0802547
; Patent No. 5780611
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT EXPRESSION OF
; TITLE OF INVENTION: COLLAGEN GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: MO USA
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,547
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 24129-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816-474-9050
; TELEFAX: 816-474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 26 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; POSITION IN GENOME:
;; UNITS: bp
US-08-802-547-2

Query Match 64.2%; Score 12.2; DB 2; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 47
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; Sequence 2, Application US/08712357
; Patent No. 5808037
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT
; TITLE OF INVENTION: EXPRESSION OF COLLAGEN GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,357
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; POSITION IN GENOME:
; UNITS: bp
US-08-712-357-2

Query Match 64.2%; Score 12.2; DB 2; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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; Sequence 4, Application US/09460555
; Patent No. 6563014
; GENERAL INFORMATION:
; APPLICANT: Albert Einstein College of Medicine of Yeshiva University
; APPLICANT: Goldstein, Harris
; APPLICANT: Paul, Jessie B.
; TITLE OF INVENTION: SELF-CONTAINED SYSTEM FOR SUSTAINED VIRAL REPLICATION
; FILE REFERENCE: 96700/552
; CURRENT APPLICATION NUMBER: US/09/460,555
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 27
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-460-555-4

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Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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; Sequence 866, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 866
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TBXSEX11 105
US-09-304-232-866

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Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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US-09-685-256-10
; Sequence 10, Application US/09685256
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; Patent No. 6660904
; GENERAL INFORMATION:
; APPLICANT: Bryant, Joseph L.
; TITLE OF INVENTION: HIV AND CD4 TRANSGENIC ANIMALS AND USES THEREFOR
; FILE REFERENCE: 4115-150 CIP
; CURRENT APPLICATION NUMBER: US/09/685,256
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-685-256-10

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Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Search completed: October 14, 2006, 19:43:11
Job time : 117 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:43:30 ; Search time 809 Seconds
(without alignments)
288.585 Million cell updates/sec

Title: US-10-604-926A-4539

Perfect score: 19

Sequence: 1 ggagaggggggtggtgct 19

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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 23237482

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Listing first 1000 summaries

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
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- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	18	94.7	23	11	US-10-310-914A-148966	Sequence 148966, A
c 5	18	94.7	23	11	US-10-310-914A-1065883	Sequence 1065883, A
c 6	16	83.2	19	11	US-10-310-914A-148924	Sequence 148924, A
c 7	15.8	83.2	19	11	US-10-310-914A-129493	Sequence 129493, A
c 8	15.8	83.2	19	11	US-10-310-914A-572030	Sequence 572030, A
c 9	15.8	83.2	22	11	US-10-310-914A-910792	Sequence 910792, A
c 10	15.8	83.2	23	11	US-10-310-914A-129473	Sequence 129473, A
c 11	15.8	83.2	23	11	US-10-310-914A-203215	Sequence 203215, A
c 12	15.8	83.2	24	11	US-10-310-914A-203187	Sequence 203187, A
c 13	15.4	81.1	18	11	US-10-310-914A-869326	Sequence 869326, A
c 14	15	78.9	18	11	US-10-310-914A-1065866	Sequence 1065866, A
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c 16	15	78.9	22	11	US-10-310-914A-1065867	Sequence 1065867, A
c 17	14.8	77.9	19	11	US-10-310-914A-203240	Sequence 203240, A

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Sequence 184336, A	25	13	US-11-060-756-184336
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c 127	13.8	72.6	23	11	US-10-310-914A-360266	Sequence 360266,	c 200	13.4	70.5	19	15	US-11-101-244-1188461	Sequence 1188461,
c 128	13.8	72.6	23	11	US-10-310-914A-577703	Sequence 577703,	c 201	13.4	70.5	19	15	US-10-310-914A-97281	Sequence 97281, A
c 129	13.8	72.6	23	11	US-10-310-914A-663881	Sequence 663881,	c 202	13.4	70.5	20	11	US-10-310-914A-100303	Sequence 100303,
c 130	13.8	72.6	23	11	US-10-310-914A-705003	Sequence 705003,	c 203	13.4	70.5	20	11	US-10-310-914A-307663	Sequence 307663,
c 131	13.8	72.6	23	11	US-10-310-914A-705010	Sequence 705010,	c 204	13.4	70.5	20	11	US-10-310-914A-307686	Sequence 307686,
c 132	13.8	72.6	23	11	US-10-310-914A-901219	Sequence 901219,	c 206	13.4	70.5	20	11	US-10-310-914A-307687	Sequence 307687,
c 133	13.8	72.6	23	11	US-10-310-914A-961700	Sequence 961700,	c 207	13.4	70.5	20	11	US-10-310-914A-416998	Sequence 416998,
c 134	13.8	72.6	23	11	US-10-310-914A-1052365	Sequence 1052365,	c 208	13.4	70.5	20	11	US-10-310-914A-455873	Sequence 455873,
c 135	13.8	72.6	24	11	US-10-310-914A-213800	Sequence 213800,	c 209	13.4	70.5	20	11	US-10-310-914A-669347	Sequence 669347,
c 136	13.8	72.6	24	11	US-10-310-914A-213805	Sequence 213805,	c 210	13.4	70.5	20	11	US-10-310-914A-808545	Sequence 808545,
c 137	13.8	72.6	24	11	US-10-310-914A-257978	Sequence 257978,	c 211	13.4	70.5	20	11	US-10-310-914A-910802	Sequence 910802,
c 138	13.8	72.6	24	11	US-10-310-914A-482250	Sequence 482250,	c 212	13.4	70.5	20	11	US-10-310-914A-73953	Sequence 73953, A
c 139	13.8	72.6	24	11	US-10-310-914A-562342	Sequence 562342,	c 213	13.4	70.5	21	11	US-10-310-914A-84238	Sequence 84238, A
c 140	13.8	72.6	24	11	US-10-310-914A-562351	Sequence 562351,	c 214	13.4	70.5	21	11	US-10-310-914A-74063	Sequence 74063, A
c 141	13.8	72.6	24	11	US-10-310-914A-705014	Sequence 705014,	c 215	13.4	70.5	21	11	US-10-310-914A-84238	Sequence 84238, A
c 142	13.8	72.6	24	11	US-10-310-914A-705042	Sequence 705042,	c 216	13.4	70.5	21	11	US-10-310-914A-97278	Sequence 97278, A
c 143	13.8	72.6	24	11	US-10-310-914A-811880	Sequence 811880,	c 217	13.4	70.5	21	11	US-10-310-914A-455893	Sequence 455893,
c 144	13.8	72.6	25	8	US-10-719-956-498100	Sequence 498100,	c 218	13.4	70.5	21	11	US-10-310-914A-73954	Sequence 73954, A
c 145	13.8	72.6	25	10	US-10-750-185-6472	Sequence 7642, Ap	c 219	13.4	70.5	21	11	US-10-310-914A-166169	Sequence 166169,
c 146	13.8	72.6	25	10	US-10-750-185-8473	Sequence 8473, Ap	c 220	13.4	70.5	21	11	US-10-310-914A-663464	Sequence 663464,
c 147	13.8	72.6	25	10	US-10-750-623-7642	Sequence 7642, Ap	c 221	13.4	70.5	21	11	US-10-310-914A-669353	Sequence 669353,
c 148	13.8	72.6	25	10	US-10-750-623-8473	Sequence 8473, Ap	c 222	13.4	70.5	21	11	US-10-310-914A-669355	Sequence 669355,
c 149	13.8	72.6	25	11	US-10-310-914A-97244	Sequence 97244, A	c 223	13.4	70.5	21	11	US-10-310-914A-1011823	Sequence 1011823,
c 150	13.8	72.6	25	11	US-10-310-914A-213820	Sequence 213820,	c 224	13.4	70.5	22	11	US-10-310-914A-1037133	Sequence 1037133,
c 151	13.8	72.6	25	11	US-10-310-914A-213820	Sequence 213820,	c 225	13.4	70.5	22	11	US-10-310-914A-1058183	Sequence 1058183,
c 152	13.8	72.6	25	11	US-10-310-914A-385338	Sequence 385338,	c 226	13.4	70.5	22	11	US-10-310-914A-454990	Sequence 454990,
c 153	13.8	72.6	25	13	US-11-060-756-134938	Sequence 134938,	c 227	13.4	70.5	22	11	US-10-310-914A-455793	Sequence 455793,
c 154	13.8	72.6	25	13	US-11-060-756-194392	Sequence 194392,	c 228	13.4	70.5	22	11	US-10-310-914A-455874	Sequence 455874,
c 155	13.8	72.6	25	15	US-11-121-849-468319	Sequence 468319,	c 229	13.4	70.5	22	11	US-10-310-914A-777833	Sequence 777833,
c 156	13.8	72.6	26	11	US-10-310-914A-705043	Sequence 705043,	c 230	13.4	70.5	22	11	US-10-310-914A-1037133	Sequence 1037133,
c 157	13.8	72.6	27	11	US-10-310-914A-294431	Sequence 294431,	c 231	13.4	70.5	23	11	US-10-310-914A-74064	Sequence 74064, A
c 158	13.8	72.6	27	11	US-10-310-914A-294596	Sequence 294596,	c 232	13.4	70.5	23	11	US-10-310-914A-213803	Sequence 213803,
c 159	13.8	72.6	27	11	US-10-310-914A-294779	Sequence 294779,	c 233	13.4	70.5	23	11	US-10-310-914A-216869	Sequence 216869,
c 160	13.8	72.6	27	11	US-10-310-914A-294963	Sequence 294963,	c 234	13.4	70.5	23	11	US-10-310-914A-216870	Sequence 216870,
c 161	13.8	72.6	27	11	US-10-310-914A-295292	Sequence 295292,	c 235	13.4	70.5	23	11	US-10-310-914A-388921	Sequence 388921,
c 162	13.8	72.6	27	11	US-10-310-914A-295446	Sequence 295446,	c 236	13.4	70.5	23	11	US-10-310-914A-388921	Sequence 388921,
c 163	13.8	72.6	27	11	US-10-310-914A-295598	Sequence 295598,						US-10-310-914A-777805	Sequence 777805,

237	13.4	70.5	23	11	US-10-310-914A-777822	Sequence 777822,	310	13.2	69.5	25	10	US-10-956-157-229682	Sequence 229682,
238	13.4	70.5	23	11	US-10-310-914A-1025782	Sequence 1025782,	311	13.2	69.5	25	10	US-10-956-157-229683	Sequence 229683,
239	13.4	70.5	24	11	US-10-310-914A-97243	Sequence 97243, A	312	13.2	69.5	25	10	US-10-956-157-229684	Sequence 229684,
240	13.4	70.5	24	11	US-10-310-914A-735904	Sequence 735904,	313	13.2	69.5	25	11	US-10-310-914A-136854	Sequence 136854,
241	13.4	70.5	24	11	US-10-310-914A-959232	Sequence 959232,	314	13.2	69.5	25	11	US-10-310-914A-659406	Sequence 659406,
242	13.4	70.5	25	11	US-10-310-914A-388925	Sequence 388925,	315	13.2	69.5	25	11	US-10-310-914A-1154445	Sequence 1154445,
243	13.4	70.5	27	11	US-10-310-914A-434377	Sequence 434377,	316	13.2	69.5	25	13	US-11-036-317-178245	Sequence 178245,
244	13.2	69.5	18	7	US-10-349-143-9827	Sequence 9827, Ap	317	13.2	69.5	25	13	US-11-036-317-183808	Sequence 183808,
245	13.2	69.5	18	11	US-10-310-914A-115803	Sequence 115803,	318	13.2	69.5	25	13	US-11-036-317-247130	Sequence 247130,
246	13.2	69.5	18	11	US-10-310-914A-442574	Sequence 442574,	319	13.2	69.5	25	13	US-11-036-317-256038	Sequence 256038,
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248	13.2	69.5	18	11	US-10-310-914A-963834	Sequence 963834,	321	13.2	69.5	25	13	US-11-036-317-291683	Sequence 291683,
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252	13.2	69.5	19	11	US-10-310-914A-195423	Sequence 195423,	325	13.2	69.5	25	13	US-11-036-317-864691	Sequence 864691,
253	13.2	69.5	19	11	US-10-310-914A-290076	Sequence 290076,	326	13.2	69.5	25	13	US-11-036-317-908932	Sequence 908932,
254	13.2	69.5	19	11	US-10-310-914A-841604	Sequence 841604,	327	13.2	69.5	25	13	US-11-036-317-929668	Sequence 929668,
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256	13.2	69.5	19	14	US-11-083-784-790058	Sequence 790058,	329	13.2	69.5	25	13	US-11-036-317-980151	Sequence 980151,
257	13.2	69.5	19	14	US-11-083-784-1577418	Sequence 1577418,	330	13.2	69.5	25	15	US-11-121-849-29929	Sequence 29929, A
258	13.2	69.5	19	15	US-11-101-244-790058	Sequence 790058,	331	13.2	69.5	25	15	US-11-121-849-91257	Sequence 91257, A
259	13.2	69.5	19	15	US-11-101-244-1577418	Sequence 1577418,	332	13.2	69.5	25	15	US-11-121-849-91257	Sequence 91257, A
260	13.2	69.5	20	7	US-10-352-179-24	Sequence 24, Appl	333	13.2	69.5	25	16	US-11-136-527-222834	Sequence 222834,
261	13.2	69.5	20	11	US-10-310-914A-261339	Sequence 261339,	334	13.2	69.5	25	16	US-11-136-527-222839	Sequence 222839,
262	13.2	69.5	20	11	US-10-310-914A-649974	Sequence 649974,	335	13.2	69.5	26	11	US-10-310-914A-1154412	Sequence 1154412,
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264	13.2	69.5	20	11	US-10-310-914A-720599	Sequence 720599,	337	13.2	69.5	28	11	US-10-310-914A-824017	Sequence 824017,
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270	13.2	69.5	21	11	US-10-310-914A-195613	Sequence 195613,	343	13	69.5	18	11	US-10-310-914A-343565	Sequence 343565,
271	13.2	69.5	21	11	US-10-310-914A-281171	Sequence 281171,	344	13	69.5	18	11	US-10-310-914A-613668	Sequence 613668,
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276	13.2	69.5	21	11	US-10-310-914A-841608	Sequence 841608,	349	13	69.5	20	11	US-10-310-914A-1277951	Sequence 1277951,
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291	13.2	69.5	23	11	US-10-310-914A-334910	Sequence 334910,	364	12.8	67.4	18	11	US-10-310-914A-873278	Sequence 873278,
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298	13.2	69.5	23	11	US-10-310-914A-976914	Sequence 976914,	371	12.8	67.4	19	11	US-10-310-914A-474111	Sequence 474111,
299	13.2	69.5	24	11	US-10-310-914A-1154444	Sequence 1154444,	372	12.8	67.4	19	11	US-10-310-914A-500548	Sequence 500548,
300	13.2	69.5	24	11	US-10-310-914A-115836	Sequence 115836,	373	12.8	67.4	19	11	US-10-310-914A-577702	Sequence 577702,
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302	13.2	69.5	24	11	US-10-310-914A-326330	Sequence 326330,	375	12.8	67.4	19	11	US-10-310-914A-847855	Sequence 847855,
303	13.2	69.5	24	11	US-10-310-914A-619989	Sequence 619989,	376	12.8	67.4	19	11	US-10-310-914A-1093299	Sequence 1093299,
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C 385	12.8	67.4	19 15	US-11-101-244-487336	Sequence 487336,	c 458	12.8	67.4	25 13	US-11-036-317-655548	Sequence 655548,
C 386	12.8	67.4	19 15	US-11-101-244-487412	Sequence 487412,	c 459	12.8	67.4	25 13	US-11-060-756-134993	Sequence 134993,
C 387	12.8	67.4	19 15	US-11-101-244-487412	Sequence 487412,	c 460	12.8	67.4	25 13	US-11-060-756-170180	Sequence 170180,
388	12.8	67.4	19 15	US-11-101-244-715680	Sequence 715680,	461	12.8	67.4	25 13	US-11-060-756-170181	Sequence 170181,
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390	12.8	67.4	19 15	US-11-101-244-1563591	Sequence 1563591,	463	12.8	67.4	25 13	US-11-060-756-212339	Sequence 212339,
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591	12.6	66.3	23	11	US-10-310-914A-610381	Sequence 610381, A	c 664	12.6	66.3	25	15	US-10-310-914A-1242802	Sequence 1242802, A
592	12.6	66.3	23	11	US-10-310-914A-610409	Sequence 610409, A	c 665	12.6	66.3	25	15	US-10-310-914A-1358454	Sequence 1358454, A
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c 676	12.4	65.3	17	3	US-09-928-412-4	Sequence 4, Appli	749	12.4	65.3	20	11	US-10-310-914A-259788	Sequence 259788,
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c 680	12.4	65.3	18	11	US-10-310-914A-347205	Sequence 347205,	c 753	12.4	65.3	20	11	US-10-310-914A-426679	Sequence 426679,
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c 682	12.4	65.3	18	11	US-10-310-914A-388943	Sequence 388943,	755	12.4	65.3	20	11	US-10-310-914A-508685	Sequence 508685,
c 683	12.4	65.3	18	11	US-10-310-914A-426678	Sequence 426678,	756	12.4	65.3	20	11	US-10-310-914A-589172	Sequence 589172,
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c 688	12.4	65.3	18	11	US-10-310-914A-747691	Sequence 747691,	761	12.4	65.3	20	11	US-10-310-914A-1141416	Sequence 1141416,
c 689	12.4	65.3	18	11	US-10-310-914A-828958	Sequence 828958,	762	12.4	65.3	20	11	US-10-310-914A-1202746	Sequence 1202746,
c 690	12.4	65.3	18	11	US-10-310-914A-973242	Sequence 973242,	763	12.4	65.3	20	11	US-10-310-914A-1214372	Sequence 1214372,
c 691	12.4	65.3	18	11	US-10-310-914A-1126495	Sequence 1126495,	764	12.4	65.3	20	11	US-10-310-914A-1297947	Sequence 1297947,
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c 693	12.4	65.3	19	10	US-10-923-142-189	Sequence 189, App	766	12.4	65.3	21	11	US-10-310-914A-158126	Sequence 158126,
c 694	12.4	65.3	19	10	US-10-206-693-542	Sequence 542, App	767	12.4	65.3	21	11	US-10-310-914A-205419	Sequence 205419,
c 695	12.4	65.3	19	10	US-10-206-693-641	Sequence 641, App	768	12.4	65.3	21	11	US-10-310-914A-211298	Sequence 211298,
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c 697	12.4	65.3	19	11	US-10-310-914A-235785	Sequence 235785,	c 770	12.4	65.3	21	11	US-10-310-914A-465754	Sequence 465754,
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c 707	12.4	65.3	19	11	US-10-310-914A-799511	Sequence 799511,	c 780	12.4	65.3	21	11	US-10-310-914A-986072	Sequence 986072,
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c 715	12.4	65.3	19	11	US-10-310-914A-1123421	Sequence 1123421,	788	12.4	65.3	22	10	US-10-924-375-42	Sequence 42, Appl
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c 718	12.4	65.3	19	11	US-10-310-914A-1181241	Sequence 1181241,	c 791	12.4	65.3	22	11	US-10-310-914A-421652	Sequence 421652,
c 719	12.4	65.3	19	11	US-10-310-914A-1212713	Sequence 1212713,	c 792	12.4	65.3	22	11	US-10-310-914A-465703	Sequence 465703,
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c 726	12.4	65.3	19	14	US-11-083-784-897923	Sequence 897923,	c 799	12.4	65.3	22	11	US-10-310-914A-988803	Sequence 988803,
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c 734	12.4	65.3	19	15	US-11-101-244-337264	Sequence 337264,	c 807	12.4	65.3	23	11	US-10-310-914A-310976	Sequence 310976,
c 735	12.4	65.3	19	15	US-11-101-244-386301	Sequence 386301,	c 808	12.4	65.3	23	11	US-10-310-914A-375059	Sequence 375059,
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c 745	12.4	65.3	19	15	US-11-101-244-1563590	Sequence 1563590,	c 818	12.4	65.3	23	11	US-10-310-914A-801182	Sequence 801182,
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c 747	12.4	65.3	20	11	US-10-310-914A-133701	Sequence 133701,	c 820	12.4	65.3	23	11	US-10-310-914A-889969	Sequence 889969,

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c 823	12.4	65.3	24	11	US-10-310-914A-224236	Sequence 224236, A	c 896	12.4	65.3	27	8	US-10-673-127-191	Sequence 191, App
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c 828	12.4	65.3	24	11	US-10-310-914A-747613	Sequence 747613, A	c 901	12.4	65.3	27	10	US-10-671-411-191	Sequence 191, App
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c 830	12.4	65.3	24	11	US-10-310-914A-966493	Sequence 966493, A	c 903	12.4	65.3	27	10	US-10-671-106-191	Sequence 191, App
c 831	12.4	65.3	24	11	US-10-310-914A-988774	Sequence 988774, A	c 904	12.4	65.3	27	11	US-10-310-914A-465702	Sequence 1100958, A
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835	12.4	65.3	25	10	US-10-750-185-6814	Sequence 6814, App	c 908	12.4	65.3	30	7	US-10-437-708-10	Sequence 10, App
c 836	12.4	65.3	25	10	US-10-750-623-6814	Sequence 6814, App	c 909	12.4	65.3	30	7	US-10-437-708-38	Sequence 38, App
c 837	12.4	65.3	25	11	US-10-310-914A-133635	Sequence 133635, A	c 910	12.4	65.3	30	7	US-10-395-402-10	Sequence 10, App
838	12.4	65.3	25	11	US-10-310-914A-307665	Sequence 307665, A	c 911	12.4	65.3	30	7	US-10-395-402-38	Sequence 38, App
839	12.4	65.3	25	11	US-10-310-914A-426729	Sequence 426729, A	c 912	12.4	65.3	30	7	US-10-395-402-39	Sequence 39, App
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c 841	12.4	65.3	25	11	US-10-310-914A-465744	Sequence 465744, A	c 914	12.4	65.3	30	9	US-10-257-199-10	Sequence 10, App
c 842	12.4	65.3	25	11	US-10-310-914A-488245	Sequence 488245, A	c 915	12.4	65.3	30	9	US-10-257-199-38	Sequence 38, App
c 843	12.4	65.3	25	11	US-10-310-914A-510943	Sequence 510943, A	c 916	12.4	65.3	30	9	US-10-257-199-39	Sequence 39, App
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c 967 12.2 64.2 19 11 US-10-310-914A-535859 Sequence 535859,
c 968 12.2 64.2 19 11 US-10-310-914A-550076 Sequence 550076,
c 969 12.2 64.2 19 11 US-10-310-914A-643942 Sequence 643942,
c 970 12.2 64.2 19 11 US-10-310-914A-732531 Sequence 732531,
c 971 12.2 64.2 19 11 US-10-310-914A-735139 Sequence 735139,
c 972 12.2 64.2 19 11 US-10-310-914A-735140 Sequence 735140,
c 973 12.2 64.2 19 11 US-10-310-914A-741358 Sequence 741358,
c 974 12.2 64.2 19 11 US-10-310-914A-765387 Sequence 765387,
c 975 12.2 64.2 19 11 US-10-310-914A-774771 Sequence 774771,
c 976 12.2 64.2 19 11 US-10-310-914A-833761 Sequence 833761,
c 977 12.2 64.2 19 11 US-10-310-914A-854200 Sequence 854200,
c 978 12.2 64.2 19 11 US-10-310-914A-876219 Sequence 876219,
c 979 12.2 64.2 19 11 US-10-310-914A-880636 Sequence 880636,
c 980 12.2 64.2 19 11 US-10-310-914A-880705 Sequence 880705,
c 981 12.2 64.2 19 11 US-10-310-914A-916252 Sequence 916252,
c 982 12.2 64.2 19 11 US-10-310-914A-922088 Sequence 922088,
c 983 12.2 64.2 19 11 US-10-310-914A-939711 Sequence 939711,
c 984 12.2 64.2 19 11 US-10-310-914A-991974 Sequence 991974,
c 985 12.2 64.2 19 11 US-10-310-914A-1069554 Sequence 1069554,
c 986 12.2 64.2 19 11 US-10-310-914A-1078919 Sequence 1078919,
c 987 12.2 64.2 19 11 US-10-310-914A-1093321 Sequence 1093321,
c 988 12.2 64.2 19 11 US-10-310-914A-1099644 Sequence 1099644,
c 989 12.2 64.2 19 11 US-10-310-914A-1126557 Sequence 1126557,
c 990 12.2 64.2 19 11 US-10-310-914A-1139647 Sequence 1139647,
c 991 12.2 64.2 19 11 US-10-310-914A-1178997 Sequence 1178997,
c 992 12.2 64.2 19 11 US-10-310-914A-1211302 Sequence 1211302,
c 993 12.2 64.2 19 11 US-10-310-914A-1306779 Sequence 1306779,
c 994 12.2 64.2 19 11 US-10-310-914A-1306852 Sequence 1306852,
c 995 12.2 64.2 19 11 US-10-310-914A-1370003 Sequence 1370003,
c 996 12.2 64.2 19 11 US-10-310-914A-1381444 Sequence 1381444,
c 997 12.2 64.2 19 14 US-11-083-784-9345 Sequence 9345, Ap
c 998 12.2 64.2 19 14 US-11-083-784-88104 Sequence 88104, A
c 999 12.2 64.2 19 14 US-11-083-784-116412 Sequence 116412,
c1000 12.2 64.2 19 14 US-11-083-784-128169 Sequence 128169,
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ALIGNMENTS

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RESULT 1
US-10-310-914A-35144
; Sequence 35144, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35144
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-35144
Query Match 100.0%; Score 19; DB 11; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
|||||
Db 1 GGAGAGGGGGTGGGTGCT 19
|||||

RESULT 2
US-10-310-914A-1065850/c
; Sequence 1065850, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148934
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148934
Query Match 100.0%; Score 19; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
|||||
Db 20 GGAGAGGGGGTGGGTGCT 2
|||||

RESULT 4
US-10-310-914A-148966/c
; Sequence 148966, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148966
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148966
```

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; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065850
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065850
Query Match 100.0%; Score 19; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
|||||
Db 19 GGAGAGGGGGTGGGTGCT 1
|||||

RESULT 3
US-10-310-914A-148934/c
; Sequence 148934, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148934
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148934
Query Match 100.0%; Score 19; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
|||||
Db 20 GGAGAGGGGGTGGGTGCT 2
|||||

RESULT 4
US-10-310-914A-148966/c
; Sequence 148966, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148966
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148966
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Query Match 94.7%; Score 18; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGTGCT 18
|||||
Db 18 GGAGAAGGGGGTGGTGCT 1

RESULT 5

US-10-310-914A-1065883/c
; Sequence 1065883, Application US/10310914A
; Publication No. US20060003322A1

GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065883
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-1065883

Query Match 94.7%; Score 18; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGTGCT 18
|||||
Db 18 GGAGAAGGGGGTGGTGCT 1

RESULT 6

US-10-310-914A-148924/c
; Sequence 148924, Application US/10310914A
; Publication No. US20060003322A1

GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148924
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-148924

Query Match 84.2%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGT 16
|||||
Db 16 GGAGAAGGGGGTGGGT 1

RESULT 7

US-10-310-914A-129493
; Sequence 129493, Application US/10310914A
; Publication No. US20060003322A1

GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129493
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-129493

Query Match 83.2%; Score 15.8; DB 11; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.9e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGTGCT 19
|||||
Db 1 GGAGAAGGGGGTGGTGCT 19

RESULT 8

US-10-310-914A-572030
; Sequence 572030, Application US/10310914A
; Publication No. US20060003322A1

GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 572030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-572030

Query Match 83.2%; Score 15.8; DB 11; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.9e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGTGCT 19
|||||
Db 1 GGAGAAGGGGGTGGTGCT 19

RESULT 9

US-10-310-914A-910792/c
; Sequence 910792, Application US/10310914A
; Publication No. US20060003322A1

GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 910792
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-910792

Query Match 83.2%; Score 15.8; DB 11; Length 22;

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; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203187
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-203187

Query Match      83.2%; Score 15.8; DB 11; Length 24;
Best Local Similarity 89.5%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
    ||| ||||| ||||| |||
Db 19 GGAGCAGGGGTGGGTCT 1

RESULT 10
US-10-310-914A-129473
; Sequence 129473, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129473
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-129473

Query Match      83.2%; Score 15.8; DB 11; Length 23;
Best Local Similarity 73.7%; Pred. No. 2.8e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
    ||| ||||| ||||| |||
Db 2 GGAGGAGGGGAGGUGGCT 20

RESULT 11
US-10-310-914A-203215/c
; Sequence 203215, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203215
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-203215

Query Match      83.2%; Score 15.8; DB 11; Length 23;
Best Local Similarity 89.5%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
    ||| ||||| ||||| |||
Db 22 GGGGAGGGGTGGGTGCT 4

RESULT 12
US-10-914A-203187/c
; Sequence 203187, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
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; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203187
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-203187

Query Match      83.2%; Score 15.8; DB 11; Length 24;
Best Local Similarity 89.5%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
    ||| ||||| ||||| |||
Db 19 GGGGAGGGGTGGGTGCT 1

RESULT 13
US-10-310-914A-869326
; Sequence 869326, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 869326
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-869326

Query Match      81.1%; Score 15.4; DB 11; Length 18;
Best Local Similarity 82.4%; Pred. No. 4.4e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTG 17
    ||| ||||| ||||| |||
Db 1 GGCAGAGGGGGUGGUG 17

RESULT 14
US-10-310-914A-1065866/c
; Sequence 1065866, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065866
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065866

Query Match      78.9%; Score 15; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGGG 15
|||||
Db 15 GGAGAAGGGGTGGG 1

RESULT 15
US-10-310-914A-148939/c
; Sequence 148939, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148939
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148939

Query Match 78.9%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGGG 15
|||||
Db 15 GGAGAAGGGGTGGG 1

RESULT 16
US-10-310-914A-1065867/c
; Sequence 1065867, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065867
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065867

Query Match 78.9%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGGG 15
|||||
Db 15 GGAGAAGGGGTGGG 1

RESULT 17
US-10-310-914A-203240/c
; Sequence 203240, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203240
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-203240

Query Match 77.9%; Score 14.8; DB 11; Length 19;
Best Local Similarity 88.9%; Pred. No. 7.9e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGGGTGC 18
|||||
Db 18 GGGAAGGGGTGGGTGC 1

RESULT 18
US-10-310-914A-1058248
; Sequence 1058248, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1058248
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1058248

Query Match 77.9%; Score 14.8; DB 11; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.9e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAAGGGGTGGGTGCT 19
|||||
Db 1 GAGAAGGGGTGGGTGCT 18

RESULT 19
US-10-310-914A-203210/c
; Sequence 203210, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203210
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-203210

Query Match 77.9%; Score 14.8; DB 11; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.9e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy      2 GAGAGGGGGTGGGTGCT 19
      | ||||| ||||| |||||
Db      20 GGAAGGGGTGGGTGCT 3

RESULT 20
US-10-310-914A-224190/c
; Sequence 224190, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 224190
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-224190

Query Match      77.9%; Score 14.8; DB 11; Length 21;
Best Local Similarity 88.9%; Pred. No. 7.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GAGAGGGGGTGGGTGCT 19
      | ||||| ||||| |||||
Db      19 GAGAAGGGGGTGAAGTGGT 2

RESULT 21
US-10-310-914A-910812/c
; Sequence 910812, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 910812
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-910812

Query Match      77.9%; Score 14.8; DB 11; Length 22;
Best Local Similarity 88.9%; Pred. No. 7.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGGGTGC 18
      | ||||| ||||| |||||
Db      18 GGAGAGGGGGTGGGTTC 1

RESULT 22
US-11-060-756-184336
; Sequence 184336, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AML101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233127
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-233127

Query Match      77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

; FILE REFERENCE: AML101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 184336
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-184336

Query Match      77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GAGAGGGGGTGGGTGCT 19
      | ||||| ||||| |||||
Db      5 GAGAAGGGGGTGAAGTGGT 22

RESULT 23
US-11-060-756-223194
; Sequence 223194, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AML101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 223194
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-223194

Query Match      77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GAGAGGGGGTGGGTGCT 19
      | ||||| ||||| |||||
Db      1 GAGAAGGGGGTGAAGTGGT 18

RESULT 24
US-11-060-756-233127
; Sequence 233127, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AML101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233127
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-233127

Query Match      77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```


QY 2 GAGAGGGGGTGGTGCT 19
|||||
Db 4 GAGAGGGGGTGAGTGCT 21

RESULT 25

US-11-060-756-269887
; Sequence 269887, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 269887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-269887

Query Match 77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
|||||
Db 2 GAGAGGGGGTGAGTGCT 19

RESULT 26

US-11-060-756-302280
; Sequence 302280, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 302280
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-302280

Query Match 77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
|||||
Db 3 GAGAGGGGGTGAGTGCT 20

RESULT 27

US-10-310-914A-491217/c
; Sequence 491217, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 491217
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-491217

Query Match 75.8%; Score 14.4; DB 11; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGGT 16
|||||
Db 16 GGAGAGGGGGTGGGT 1

RESULT 28

US-10-310-914A-224205/c
; Sequence 224205, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 224205
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-224205

Query Match 75.8%; Score 14.4; DB 11; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTG 17
|||||
Db 17 GAGAGGGGGTGAGTG 2

RESULT 29

US-10-310-914A-491213/c
; Sequence 491213, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 491213
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-491213

Query Match 75.8%; Score 14.4; DB 11; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGGT 16

Db 17 GGAGGAGGGGGTGGGT 2
||||| ||||| ||||| |||||
RESULT 30
US-10-310-914A-910789/c
; Sequence 910789, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 910789
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-910789
Query Match 75.8%; Score 14.4; DB 11; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAGAAGGGGGTGGGT 16
||||| ||||| ||||| |||||
Db 16 GGAGCAGGGGGTGGGT 1
RESULT 31
US-10-310-914A-910790/c
; Sequence 910790, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 910790
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-910790
Query Match 75.8%; Score 14.4; DB 11; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAGAAGGGGGTGGGT 16
||||| ||||| ||||| |||||
Db 16 GGAGCAGGGGGTGGGT 1
RESULT 32
US-10-310-914A-289813
; Sequence 289813, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 289813
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-289813
Query Match 75.8%; Score 14.4; DB 11; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 GAGAAGGGGGTGGGTG 17
||||| ||||| ||||| |||||
Db 4 GAGAAGUGGGUGGUG 19
RESULT 33
US-10-310-914A-455081
; Sequence 455081, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 455081
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-455081
Query Match 75.8%; Score 14.4; DB 11; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 GAGAAGGGGGTGGGTG 17
||||| ||||| ||||| |||||
Db 9 GAGAAGGGGUGGCGAG 24
RESULT 34
US-10-310-914A-856024
; Sequence 856024, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 856024
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-856024
Query Match 75.8%; Score 14.4; DB 11; Length 24;
Best Local Similarity 81.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAGAAGGGGGTGGGT 16
||||| ||||| ||||| |||||

Db 7 GGAGGAGGGGGGUGGCU 22

RESULT 35

US-10-310-914A-986078/c
; Sequence 986078, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 986078

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-986078

Query Match 75.8%; Score 14.4; DB 11; Length 24;

Best Local Similarity 93.8%; Pred. No. 1.2e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGT 16

||||| ||||| |||||

Db 20 GGACAAGGGGGTGGGT 5

RESULT 36

US-10-310-914A-939254
; Sequence 939254, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 939254

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-939254

Query Match 74.7%; Score 14.2; DB 11; Length 19;

Best Local Similarity 73.7%; Pred. No. 1.5e+04;

Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTGCT 19

||||| ||||| |||||

Db 1 GGAGAGCGGGGUGGCGGCU 19

RESULT 37

US-10-310-914A-1039501
; Sequence 1039501, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1039501

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1039501

Query Match 74.7%; Score 14.2; DB 11; Length 19;

Best Local Similarity 78.9%; Pred. No. 1.5e+04;

Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTGCT 19

||||| ||||| |||||

Db 1 GGAGAAGGGGGGCGCGGCU 19

RESULT 38

US-10-310-914A-1039502

; Sequence 1039502, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1039502

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1039502

Query Match 74.7%; Score 14.2; DB 11; Length 19;

Best Local Similarity 78.9%; Pred. No. 1.5e+04;

Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTGCT 19

||||| ||||| |||||

Db 1 GGAGAAGGGGGGCGGUGGCU 19

RESULT 39

US-10-310-914A-1051671

; Sequence 1051671, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1051671

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1051671

Query Match 74.7%; Score 14.2; DB 11; Length 19;

Best Local Similarity 73.7%; Pred. No. 1.5e+04;

Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTGCT 19

||||| ||||| |||||

Db 1 GGAGGAGGAGGUGGAGGCU 19

```

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 649973
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-649973

Query Match          74.7%; Score 14.2; DB 11; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAAGGGGTGGGTGCT 19
    ||||| ||||| ||||| |||||
Db 20 GGAGCAGCGAGTGGGTGCT 2

RESULT 43
US-10-310-914A-1207983/c
; Sequence 1207983, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1207983
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1207983

Query Match          74.7%; Score 14.2; DB 11; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAAGGGGTGGGTGCT 19
    ||||| ||||| ||||| |||||
Db 20 GGAGCTGGGGTGGGAGCT 2

RESULT 44
US-10-310-914A-1112107/c
; Sequence 1112107, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1112107
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1112107

Query Match          74.7%; Score 14.2; DB 11; Length 22;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAAGGGGTGGGTGCT 19
    ||||| ||||| ||||| |||||
Db 21 GGAGACGGGGTGACTGCT 3

Qy 1 GGAGAAAGGGGTGGGTGCT 19
    ||||| ||||| ||||| |||||
Db 21 GGAGACGGGGTGACTGCT 3

```

RESULT 47
US-10-913-271-27
; Sequence 27, Application US/10913271
; Publication No. US20050003442A1

Query Match 74.7%; Score 14.2; DB 9; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 1 GGAGAACGGGGTGGTGCT 19

Job time : 826 secs

```
Db      2  GGAGCATGGGGTAGGTGCT 20

RESULT 49
US-10-913-779-27
; Sequence 27, Application US/10913779
; Publication No. US20050005329A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DELTA 4-DESATURASE GENES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 6804.US.P1
; CURRENT APPLICATION NUMBER: US/10/913,779
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/120,637
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 09/849,199
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' Nested Primer R01239
US-10-913-779-27

Query Match      74.7%; Score 14.2; DB 9; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GGAGAGGGGGTGGTGCT 19
      ||||| ||||| |||||
Db      2  GGAGCATGGGGTAGGTGCT 20

RESULT 50
US-10-310-914A-479763
; Sequence 479763, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 479763
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-479763

Query Match      74.7%; Score 14.2; DB 11; Length 27;
Best Local Similarity 73.7%; Pred. No. 1.4e+04;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Search completed: October 14, 2006, 19:57:24
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:44:42 ; Search time 122 Seconds
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Title: US-10-604-926A-4539

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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266	10.6	55.8	25	9	US-11-348-413-816512	Sequence 816512,	c 339	10.2	53.7	19	6	US-10-424-339-1375	Sequence 1375, Ap
c 267	10.6	55.8	25	9	US-11-348-413-844160	Sequence 844160,	c 340	10.2	53.7	19	6	US-10-424-339-1375	Sequence 1375, Ap
c 268	10.6	55.8	25	9	US-11-348-413-1061093	Sequence 1061093,	c 341	10.2	53.7	19	6	US-10-536-804-5	Sequence 5, Appl
c 269	10.6	55.8	25	9	US-11-348-413-1118424	Sequence 1118424,	c 342	10.2	53.7	19	6	US-10-881-580-65	Sequence 65, Appl
c 270	10.6	55.8	25	9	US-11-348-413-1118425	Sequence 1118425,	c 343	10.2	53.7	19	6	US-10-881-580-193	Sequence 193, Ap
c 271	10.6	55.8	25	9	US-11-348-413-1118426	Sequence 1118426,	c 344	10.2	53.7	19	6	US-10-825-485-167	Sequence 167, Ap
c 272	10.6	55.8	25	9	US-11-348-413-1118427	Sequence 1118427,	c 345	10.2	53.7	19	6	US-10-825-485-474	Sequence 474, Ap
c 273	10.6	55.8	25	9	US-11-348-413-1118428	Sequence 1118428,	c 346	10.2	53.7	19	6	US-10-753-718-528	Sequence 528, Ap
c 274	10.6	55.8	25	9	US-11-348-413-1118429	Sequence 1118429,	c 347	10.2	53.7	19	7	US-11-318-240-11	Sequence 11, Appl
c 275	10.6	55.8	25	9	US-11-348-413-1118430	Sequence 1118430,	c 348	10.2	53.7	19	8	US-11-251-465-591	Sequence 591, Ap
c 276	10.6	55.8	25	9	US-11-348-413-1118431	Sequence 1118431,	c 349	10.2	53.7	19	8	US-11-219-582A-23	Sequence 23, Appl
c 277	10.6	55.8	25	9	US-11-348-413-1118432	Sequence 1118432,	c 350	10.2	53.7	19	8	US-11-219-582A-25	Sequence 25, Appl
c 278	10.6	55.8	25	9	US-11-348-413-1124401	Sequence 1124401,	c 351	10.2	53.7	19	8	US-11-219-582A-27	Sequence 27, Appl
c 279	10.6	55.8	26	6	US-10-511-937-2158	Sequence 2158, Ap	c 352	10.2	53.7	19	8	US-11-219-582A-31	Sequence 31, Appl
280	10.6	55.8	26	6	US-11-350-336-26	Sequence 26, Appl	c 353	10.2	53.7	19	8	US-11-219-582A-39	Sequence 39, Appl
281	10.6	55.8	27	6	US-10-858-013-946	Sequence 946, Ap	c 354	10.2	53.7	19	8	US-11-219-582A-43	Sequence 43, Appl
282	10.6	55.8	27	6	US-10-858-013-947	Sequence 947, Ap	c 355	10.2	53.7	19	8	US-11-219-582A-45	Sequence 45, Appl
283	10.6	55.8	27	6	US-10-858-164-946	Sequence 946, Ap	c 356	10.2	53.7	19	8	US-11-219-582A-47	Sequence 47, Appl
284	10.6	55.8	27	6	US-10-858-164-947	Sequence 947, Ap	c 357	10.2	53.7	19	8	US-11-219-582A-25	Sequence 25, Appl
c 285	10.6	55.8	29	7	US-11-395-249-204	Sequence 204, Ap	c 358	10.2	53.7	19	9	US-11-219-625A-25	Sequence 25, Appl
c 286	10.6	55.8	29	7	US-11-133-075-76	Sequence 76, Appl	c 359	10.2	53.7	19	9	US-11-217-936-2950	Sequence 2950, Ap
c 287	10.6	55.8	30	7	US-11-036-257-153	Sequence 153, Ap	c 360	10.2	53.7	19	9	US-11-217-936-3177	Sequence 3177, Ap
288	10.4	54.7	18	7	US-11-370-584-7812	Sequence 7812, Ap	c 361	10.2	53.7	19	9	US-11-361-793-25	Sequence 25, Appl
289	10.4	54.7	18	8	US-11-293-697-5452	Sequence 5452, Ap	c 362	10.2	53.7	19	9	US-11-361-793-26	Sequence 26, Appl
290	10.4	54.7	19	9	US-11-217-936-425	Sequence 425, Ap	c 363	10.2	53.7	19	9	US-10-511-937-679	Sequence 679, Ap
c 291	10.4	54.7	19	9	US-11-217-936-535	Sequence 535, Ap	c 364	10.2	53.7	20	6	US-10-517-441-1027	Sequence 1027, Ap
c 292	10.4	54.7	19	9	US-11-294-621-109	Sequence 109, Ap	c 365	10.2	53.7	20	6	US-10-525-116-982	Sequence 982, Ap
c 293	10.4	54.7	20	8	US-11-189-597-8	Sequence 8, Appl	c 366	10.2	53.7	20	6	US-10-525-116-1080	Sequence 1080, Ap
c 294	10.4	54.7	20	8	US-11-301-764-125	Sequence 125, Ap	c 367	10.2	53.7	20	7	US-11-370-584-5435	Sequence 5435, Ap
c 295	10.4	54.7	23	8	US-11-283-550-1461	Sequence 1461, Ap	c 368	10.2	53.7	20	7	US-11-370-584-5858	Sequence 5858, Ap
c 296	10.4	54.7	23	8	US-11-283-550-1473	Sequence 1473, Ap	c 369	10.2	53.7	20	7	US-11-370-584-5972	Sequence 5972, Ap
c 297	10.4	54.7	25	8	US-11-217-529-11019	Sequence 11019, A	c 370	10.2	53.7	20	7	US-11-370-584-7145	Sequence 7145, Ap
c 298	10.4	54.7	25	8	US-11-217-529-16737	Sequence 16737, A	c 371	10.2	53.7	20	7	US-11-370-584-10500	Sequence 10500, A
c 299	10.4	54.7	25	8	US-11-217-529-56574	Sequence 56574, A	c 372	10.2	53.7	20	7	US-11-370-584-10500	Sequence 10500, A
c 300	10.4	54.7	25	8	US-11-217-529-60077	Sequence 60077, A	c 373	10.2	53.7	20	9	US-11-293-598-14	Sequence 14, Appl
301	10.4	54.7	25	8	US-11-217-529-92657	Sequence 92657, A	c 374	10.2	53.7	20	9	US-11-207-382-153	Sequence 153, Ap
302	10.4	54.7	25	8	US-11-217-529-113705	Sequence 113705,	c 375	10.2	53.7	21	6	US-10-517-441-841	Sequence 841, Ap
303	10.4	54.7	25	9	US-11-348-413-177636	Sequence 177636,	c 376	10.2	53.7	21	6	US-10-997-086-28	Sequence 28, Appl
304	10.4	54.7	25	9	US-11-348-413-177637	Sequence 177637,	c 377	10.2	53.7	21	6	US-10-641-321-158	Sequence 158, Ap
305	10.4	54.7	25	9	US-11-348-413-177638	Sequence 177638,	c 378	10.2	53.7	21	8	US-11-251-465-592	Sequence 592, Ap
306	10.4	54.7	25	9	US-11-348-413-177639	Sequence 177639,	c 379	10.2	53.7	21	9	US-11-219-625A-23	Sequence 23, Appl
c 307	10.4	54.7	25	9	US-11-348-413-271160	Sequence 271160,	c 380	10.2	53.7	21	9	US-11-219-625A-24	Sequence 24, Appl
c 308	10.4	54.7	25	9	US-11-348-413-271161	Sequence 271161,	c 381	10.2	53.7	21	9	US-11-219-625A-27	Sequence 27, Appl
c 309	10.4	54.7	25	9	US-11-348-413-271162	Sequence 271162,	c 382	10.2	53.7	21	9	US-11-219-625A-28	Sequence 28, Appl
c 310	10.4	54.7	25	9	US-11-348-413-569752	Sequence 569752,	c 383	10.2	53.7	21	9	US-11-219-625A-29	Sequence 29, Appl
311	10.4	54.7	25	9	US-11-348-413-612339	Sequence 612339,	c 384	10.2	53.7	21	9	US-11-219-625A-30	Sequence 30, Appl
312	10.4	54.7	25	9	US-11-348-413-695154	Sequence 695154,	c 385	10.2	53.7	21	9	US-11-219-625A-31	Sequence 31, Appl
313	10.4	54.7	25	9	US-11-348-413-784243	Sequence 784243,	c 386	10.2	53.7	21	9	US-11-219-625A-32	Sequence 32, Appl
314	10.4	54.7	25	9	US-11-348-413-784244	Sequence 784244,	c 387	10.2	53.7	21	9	US-11-219-625A-39	Sequence 39, Appl
315	10.4	54.7	25	9	US-11-348-413-784245	Sequence 784245,	c 388	10.2	53.7	21	9	US-11-219-625A-40	Sequence 40, Appl

c 389	10.2	53.7	21	9	US-11-219-625A-43	Sequence 43, Appl	462	10.2	53.7	25	9	US-11-348-413-104405	Sequence 104405,
c 390	10.2	53.7	21	9	US-11-219-625A-44	Sequence 44, Appl	463	10.2	53.7	25	9	US-11-348-413-104406	Sequence 104406,
c 391	10.2	53.7	21	9	US-11-219-625A-45	Sequence 45, Appl	464	10.2	53.7	25	9	US-11-348-413-104407	Sequence 104407,
c 392	10.2	53.7	21	9	US-11-219-625A-46	Sequence 46, Appl	465	10.2	53.7	25	9	US-11-348-413-104408	Sequence 104408,
c 393	10.2	53.7	21	9	US-11-219-625A-47	Sequence 47, Appl	c 466	10.2	53.7	25	9	US-11-348-413-136541	Sequence 136541,
c 394	10.2	53.7	21	9	US-11-219-625A-48	Sequence 48, Appl	c 467	10.2	53.7	25	9	US-11-348-413-136542	Sequence 136542,
c 395	10.2	53.7	21	9	US-11-361-793-23	Sequence 23, Appl	468	10.2	53.7	25	9	US-11-348-413-158643	Sequence 158643,
c 396	10.2	53.7	21	9	US-11-361-793-24	Sequence 24, Appl	469	10.2	53.7	25	9	US-11-348-413-158644	Sequence 158644,
c 397	10.2	53.7	21	9	US-11-361-793-27	Sequence 27, Appl	c 470	10.2	53.7	25	9	US-11-348-413-176872	Sequence 176872,
c 398	10.2	53.7	21	9	US-11-361-793-28	Sequence 28, Appl	471	10.2	53.7	25	9	US-11-348-413-185521	Sequence 185521,
c 399	10.2	53.7	21	9	US-11-361-793-29	Sequence 29, Appl	472	10.2	53.7	25	9	US-11-348-413-185522	Sequence 185522,
c 400	10.2	53.7	21	9	US-11-361-793-30	Sequence 30, Appl	473	10.2	53.7	25	9	US-11-348-413-185523	Sequence 185523,
c 401	10.2	53.7	21	9	US-11-361-793-31	Sequence 31, Appl	474	10.2	53.7	25	9	US-11-348-413-185524	Sequence 185524,
c 402	10.2	53.7	21	9	US-11-361-793-32	Sequence 32, Appl	475	10.2	53.7	25	9	US-11-348-413-185525	Sequence 185525,
c 403	10.2	53.7	21	9	US-11-361-793-33	Sequence 33, Appl	476	10.2	53.7	25	9	US-11-348-413-185526	Sequence 185526,
c 404	10.2	53.7	21	9	US-11-361-793-39	Sequence 39, Appl	477	10.2	53.7	25	9	US-11-348-413-185527	Sequence 185527,
c 405	10.2	53.7	21	9	US-11-361-793-40	Sequence 40, Appl	478	10.2	53.7	25	9	US-11-348-413-185528	Sequence 185528,
c 406	10.2	53.7	21	9	US-11-361-793-43	Sequence 43, Appl	479	10.2	53.7	25	9	US-11-348-413-199968	Sequence 199968,
c 407	10.2	53.7	21	9	US-11-361-793-44	Sequence 44, Appl	480	10.2	53.7	25	9	US-11-348-413-199969	Sequence 199969,
c 408	10.2	53.7	21	9	US-11-361-793-45	Sequence 45, Appl	481	10.2	53.7	25	9	US-11-348-413-199970	Sequence 199970,
c 409	10.2	53.7	21	9	US-11-361-793-47	Sequence 47, Appl	482	10.2	53.7	25	9	US-11-348-413-199970	Sequence 199970,
c 410	10.2	53.7	21	9	US-11-361-793-48	Sequence 48, Appl	483	10.2	53.7	25	9	US-11-348-413-213902	Sequence 213902,
c 411	10.2	53.7	22	6	US-10-526-905-31	Sequence 31, Appl	484	10.2	53.7	25	9	US-11-348-413-213904	Sequence 213904,
c 412	10.2	53.7	22	6	US-10-526-905-31	Sequence 31, Appl	485	10.2	53.7	25	9	US-11-348-413-213905	Sequence 213905,
c 413	10.2	53.7	22	7	US-10-107-746-3	Sequence 196, App	486	10.2	53.7	25	9	US-11-348-413-213906	Sequence 213906,
c 414	10.2	53.7	23	7	US-11-340-080-81	Sequence 81, Appl	487	10.2	53.7	25	9	US-11-348-413-220778	Sequence 220778,
c 415	10.2	53.7	23	7	US-11-340-080-82	Sequence 82, Appl	488	10.2	53.7	25	9	US-11-348-413-220779	Sequence 220779,
c 416	10.2	53.7	23	7	US-11-340-080-83	Sequence 83, Appl	489	10.2	53.7	25	9	US-11-348-413-220780	Sequence 220780,
c 417	10.2	53.7	23	7	US-11-340-080-84	Sequence 84, Appl	c 490	10.2	53.7	25	9	US-11-348-413-324244	Sequence 324244,
c 418	10.2	53.7	23	7	US-11-340-080-85	Sequence 85, Appl	c 491	10.2	53.7	25	9	US-11-348-413-324245	Sequence 324245,
c 419	10.2	53.7	23	7	US-11-340-080-86	Sequence 86, Appl	c 492	10.2	53.7	25	9	US-11-348-413-324246	Sequence 324246,
c 420	10.2	53.7	23	7	US-11-340-080-87	Sequence 87, Appl	c 493	10.2	53.7	25	9	US-11-348-413-324247	Sequence 324247,
c 421	10.2	53.7	23	7	US-11-340-080-88	Sequence 88, Appl	c 494	10.2	53.7	25	9	US-11-348-413-324248	Sequence 324248,
c 422	10.2	53.7	23	7	US-11-340-080-89	Sequence 89, Appl	c 495	10.2	53.7	25	9	US-11-348-413-324249	Sequence 324249,
c 423	10.2	53.7	23	8	US-11-078-073-81	Sequence 81, Appl	c 496	10.2	53.7	25	9	US-11-348-413-324250	Sequence 324250,
c 424	10.2	53.7	23	8	US-11-078-073-82	Sequence 82, Appl	c 497	10.2	53.7	25	9	US-11-348-413-324251	Sequence 324251,
c 425	10.2	53.7	23	8	US-11-078-073-83	Sequence 83, Appl	c 498	10.2	53.7	25	9	US-11-348-413-324252	Sequence 324252,
c 426	10.2	53.7	23	8	US-11-078-073-84	Sequence 84, Appl	c 499	10.2	53.7	25	9	US-11-348-413-344067	Sequence 344067,
c 427	10.2	53.7	23	8	US-11-078-073-85	Sequence 85, Appl	c 500	10.2	53.7	25	9	US-11-348-413-344068	Sequence 344068,
c 428	10.2	53.7	23	8	US-11-078-073-86	Sequence 86, Appl	501	10.2	53.7	25	9	US-11-348-413-348889	Sequence 348889,
c 429	10.2	53.7	23	8	US-11-078-073-87	Sequence 87, Appl	502	10.2	53.7	25	9	US-11-348-413-348890	Sequence 348890,
c 430	10.2	53.7	23	8	US-11-078-073-88	Sequence 88, Appl	503	10.2	53.7	25	9	US-11-348-413-390676	Sequence 390676,
c 431	10.2	53.7	23	8	US-11-078-073-89	Sequence 89, Appl	504	10.2	53.7	25	9	US-11-348-413-410811	Sequence 410811,
c 432	10.2	53.7	24	7	US-11-095-042-7	Sequence 7, Appl	505	10.2	53.7	25	9	US-11-348-413-410812	Sequence 410812,
c 433	10.2	53.7	25	6	US-10-915-763A-10	Sequence 10, Appl	506	10.2	53.7	25	9	US-11-348-413-410813	Sequence 410813,
c 434	10.2	53.7	25	6	US-10-354-933-1011	Sequence 1011, App	507	10.2	53.7	25	9	US-11-348-413-410814	Sequence 410814,
c 435	10.2	53.7	25	7	US-11-234-676-179	Sequence 179, App	508	10.2	53.7	25	9	US-11-348-413-410815	Sequence 410815,
c 436	10.2	53.7	25	8	US-11-217-529-24718	Sequence 24718, A	509	10.2	53.7	25	9	US-11-348-413-410816	Sequence 410816,
c 437	10.2	53.7	25	8	US-11-217-529-24723	Sequence 24723, A	510	10.2	53.7	25	9	US-11-348-413-585316	Sequence 585316,
c 438	10.2	53.7	25	8	US-11-217-529-27814	Sequence 27814, A	c 511	10.2	53.7	25	9	US-11-348-413-589373	Sequence 589373,
c 439	10.2	53.7	25	8	US-11-217-529-30334	Sequence 30334, A	c 512	10.2	53.7	25	9	US-11-348-413-589374	Sequence 589374,
c 440	10.2	53.7	25	8	US-11-217-529-36261	Sequence 36261, A	c 513	10.2	53.7	25	9	US-11-348-413-592998	Sequence 592998,
c 441	10.2	53.7	25	8	US-11-217-529-41137	Sequence 41137, A	514	10.2	53.7	25	9	US-11-348-413-592999	Sequence 592999,
c 442	10.2	53.7	25	8	US-11-217-529-46756	Sequence 46756, A	515	10.2	53.7	25	9	US-11-348-413-593000	Sequence 593000,
c 443	10.2	53.7	25	8	US-11-217-529-56599	Sequence 56599, A	516	10.2	53.7	25	9	US-11-348-413-593001	Sequence 593001,
c 444	10.2	53.7	25	8	US-11-217-529-93817	Sequence 93817, A	517	10.2	53.7	25	9	US-11-348-413-593002	Sequence 593002,
c 445	10.2	53.7	25	8	US-11-217-529-104158	Sequence 104158, A	518	10.2	53.7	25	9	US-11-348-413-610218	Sequence 610218,
c 446	10.2	53.7	25	8	US-11-217-529-115602	Sequence 115602, A	519	10.2	53.7	25	9	US-11-348-413-611866	Sequence 611866,
c 447	10.2	53.7	25	8	US-11-217-529-122010	Sequence 122010, A	520	10.2	53.7	25	9	US-11-348-413-614787	Sequence 614787,
c 448	10.2	53.7	25	8	US-11-217-529-142300	Sequence 142300, A	521	10.2	53.7	25	9	US-11-348-413-650873	Sequence 650873,
c 449	10.2	53.7	25	8	US-11-217-529-145931	Sequence 145931, A	522	10.2	53.7	25	9	US-11-348-413-655630	Sequence 655630,
c 450	10.2	53.7	25	8	US-11-217-529-163015	Sequence 163015, A	523	10.2	53.7	25	9	US-11-348-413-679840	Sequence 679840,
c 451	10.2	53.7	25	9	US-11-348-413-22794	Sequence 22794, A	524	10.2	53.7	25	9	US-11-348-413-681526	Sequence 681526,
c 452	10.2	53.7	25	9	US-11-348-413-22795	Sequence 22795, A	525	10.2	53.7	25	9	US-11-348-413-696113	Sequence 696113,
c 453	10.2	53.7	25	9	US-11-348-413-22796	Sequence 22796, A	526	10.2	53.7	25	9	US-11-348-413-790424	Sequence 790424,
c 454	10.2	53.7	25	9	US-11-348-413-22797	Sequence 22797, A	527	10.2	53.7	25	9	US-11-348-413-790424	Sequence 790424,
c 455	10.2	53.7	25	9	US-11-348-413-22798	Sequence 22798, A	528	10.2	53.7	25	9	US-11-348-413-792471	Sequence 792471,
c 456	10.2	53.7	25	9	US-11-348-413-24417	Sequence 24417, A	529	10.2	53.7	25	9	US-11-348-413-792471	Sequence 792471,
c 457	10.2	53.7	25	9	US-11-348-413-27745	Sequence 27745, A	530	10.2	53.7	25	9	US-11-348-413-792472	Sequence 792472,
c 458	10.2	53.7	25	9	US-11-348-413-63429	Sequence 63429, A	531	10.2	53.7	25	9	US-11-348-413-792473	Sequence 792473,
c 459	10.2	53.7	25	9	US-11-348-413-71712	Sequence 71712, A	532	10.2	53.7	25	9	US-11-348-413-830049	Sequence 830049,
c 460	10.2	53.7	25	9	US-11-348-413-104403	Sequence 104403, A	533	10.2	53.7	25	9	US-11-348-413-837274	Sequence 837274,
c 461	10.2	53.7	25	9	US-11-348-413-104404	Sequence 104404, A	534	10.2	53.7	25	9	US-11-348-413-837274	Sequence 837274,

535	10.2	53.7	25	9	US-11-348-413-857332	Sequence 857332,	608	10	52.6	21	7	US-11-260-845-181	Sequence 181, App
536	10.2	53.7	25	9	US-11-348-413-874104	Sequence 874104,	609	10	52.6	21	7	US-11-260-845-186	Sequence 186, App
C 537	10.2	53.7	25	9	US-11-348-413-880485	Sequence 880485,	610	10	52.6	21	7	US-11-259-588-86	Sequence 86, Appl
C 538	10.2	53.7	25	9	US-11-348-413-957149	Sequence 957149,	C 611	10	52.6	21	7	US-11-084-700-121	Sequence 121, App
C 539	10.2	53.7	25	9	US-11-348-413-968628	Sequence 968628,	C 612	10	52.6	21	7	US-11-112-926-550	Sequence 550, App
C 540	10.2	53.7	25	9	US-11-348-413-985909	Sequence 985909,	C 613	10	52.6	21	9	US-11-320-440-202	Sequence 202, App
C 541	10.2	53.7	25	9	US-11-348-413-985910	Sequence 985910,	614	10	52.6	22	7	US-11-260-845-182	Sequence 182, App
C 542	10.2	53.7	25	9	US-11-348-413-995220	Sequence 995220,	615	10	52.6	22	7	US-11-389-343-794	Sequence 794, App
C 543	10.2	53.7	25	9	US-11-348-413-102706	Sequence 102706,	616	10	52.6	22	8	US-11-298-875A-61	Sequence 61, Appl
C 544	10.2	53.7	25	9	US-11-348-413-1051169	Sequence 1051169,	617	10	52.6	23	8	US-11-254-524-20	Sequence 20, Appl
C 545	10.2	53.7	25	9	US-11-348-413-1052285	Sequence 1052285,	C 618	10	52.6	23	8	US-11-283-550-1474	Sequence 1474, Ap
C 546	10.2	53.7	25	9	US-11-348-413-1124402	Sequence 1124402,	C 619	10	52.6	23	8	US-11-283-550-1475	Sequence 1475, Ap
C 547	10.2	53.7	25	9	US-11-348-413-1129371	Sequence 1129371,	C 620	10	52.6	23	8	US-11-283-550-5260	Sequence 5260, Ap
C 548	10.2	53.7	25	9	US-11-348-413-1129372	Sequence 1129372,	621	10	52.6	23	8	US-11-283-550-5261	Sequence 5261, Ap
C 549	10.2	53.7	25	9	US-11-348-413-1129373	Sequence 1129373,	622	10	52.6	23	8	US-11-283-550-5262	Sequence 5262, Ap
C 550	10.2	53.7	25	9	US-11-348-413-1160700	Sequence 1160700,	623	10	52.6	23	8	US-11-283-550-5263	Sequence 5263, Ap
C 551	10.2	53.7	25	9	US-11-348-413-1205861	Sequence 1205861,	624	10	52.6	23	8	US-11-283-550-5264	Sequence 5264, Ap
C 552	10.2	53.7	25	9	US-11-348-413-1205862	Sequence 1205862,	625	10	52.6	23	8	US-11-283-550-5265	Sequence 5265, Ap
C 553	10.2	53.7	25	9	US-11-348-413-1226558	Sequence 1226558,	C 626	10	52.6	24	6	US-10-858-013-184	Sequence 184, App
C 554	10.2	53.7	25	9	US-11-348-413-1253325	Sequence 1253325,	C 627	10	52.6	24	6	US-10-858-013-185	Sequence 185, App
C 555	10.2	53.7	25	9	US-11-348-413-1263368	Sequence 1263368,	C 628	10	52.6	24	6	US-10-858-013-186	Sequence 186, App
C 556	10.2	53.7	25	9	US-11-348-413-1263369	Sequence 1263369,	C 629	10	52.6	24	6	US-10-466-817-1	Sequence 1, Appli
C 557	10.2	53.7	25	9	US-11-348-413-1266309	Sequence 1266309,	C 630	10	52.6	24	6	US-10-858-164-184	Sequence 184, App
C 558	10.2	53.7	26	6	US-10-552-552-20	Sequence 20, Appl	C 631	10	52.6	24	6	US-10-858-164-185	Sequence 185, App
C 559	10.2	53.7	26	8	US-11-173-889-51	Sequence 51, Appl	C 632	10	52.6	24	6	US-10-858-164-186	Sequence 186, App
C 560	10.2	53.7	26	8	US-11-173-889-63	Sequence 63, Appl	C 633	10	52.6	24	6	US-10-888-359B-85	Sequence 85, Appl
C 561	10.2	53.7	26	8	US-11-173-889-78	Sequence 78, Appl	C 634	10	52.6	24	9	US-11-293-598-37	Sequence 37, Appl
C 562	10.2	53.7	27	8	US-11-200-465-5	Sequence 5, Appli	C 635	10	52.6	25	8	US-11-217-529-14012	Sequence 14012, A
C 563	10.2	53.7	27	8	US-11-223-812-5	Sequence 5, Appli	C 636	10	52.6	25	8	US-11-217-529-22553	Sequence 22553, A
C 564	10.2	53.7	28	7	US-11-234-676-193	Sequence 193, App	C 637	10	52.6	25	8	US-11-217-529-34937	Sequence 34937, A
C 565	10.2	53.7	29	9	US-11-372-250-2	Sequence 2, Appli	C 638	10	52.6	25	8	US-11-217-529-39671	Sequence 39671, A
C 566	10.2	53.7	30	8	US-11-234-676-180	Sequence 180, App	C 639	10	52.6	25	8	US-11-217-529-67056	Sequence 67056, A
C 567	10.2	53.7	30	8	US-11-238-155-29	Sequence 29, Appl	C 640	10	52.6	25	8	US-11-217-529-67117	Sequence 67117, A
C 568	10.2	53.7	30	8	US-11-238-155-35	Sequence 35, Appl	C 641	10	52.6	25	8	US-11-217-529-83862	Sequence 83862, A
C 569	10.2	53.7	30	8	US-11-238-155-37	Sequence 37, Appl	C 642	10	52.6	25	8	US-11-217-529-84700	Sequence 84700, A
C 570	10.2	53.7	30	8	US-11-238-155-39	Sequence 39, Appl	C 643	10	52.6	25	8	US-11-217-529-85590	Sequence 85590, A
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C 575	10	52.6	19	6	US-10-424-339-781	Sequence 781, App	C 648	10	52.6	25	8	US-11-217-529-113380	Sequence 113380, A
C 576	10	52.6	19	6	US-10-424-339-990	Sequence 990, App	C 649	10	52.6	25	8	US-11-217-529-114928	Sequence 114928, A
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C 580	10	52.6	19	7	US-11-299-391-931	Sequence 931, App	C 653	10	52.6	25	8	US-11-217-529-127555	Sequence 127555, A
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C 583	10	52.6	19	9	US-11-217-936-2079	Sequence 2079, Ap	C 656	10	52.6	25	8	US-11-217-529-176787	Sequence 176787, A
C 584	10	52.6	19	9	US-11-217-936-2374	Sequence 2374, Ap	C 657	10	52.6	25	8	US-11-217-529-176792	Sequence 176792, A
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C 586	10	52.6	19	9	US-11-217-936-4414	Sequence 4414, Ap	C 659	10	52.6	25	8	US-11-217-529-184124	Sequence 184124, A
C 587	10	52.6	19	9	US-11-102-087-1668	Sequence 1668, Ap	C 660	10	52.6	25	8	US-11-217-529-184131	Sequence 184131, A
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C 589	10	52.6	20	6	US-10-559-415-107	Sequence 107, App	C 662	10	52.6	25	8	US-11-217-529-185663	Sequence 185663, A
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C 592	10	52.6	20	6	US-10-668-050-107	Sequence 107, App	C 665	10	52.6	25	8	US-11-217-529-191347	Sequence 191347, A
C 593	10	52.6	20	6	US-10-668-050-108	Sequence 108, App	C 666	10	52.6	25	8	US-11-217-529-191349	Sequence 191349, A
C 594	10	52.6	20	6	US-10-668-050-109	Sequence 109, App	C 667	10	52.6	25	9	US-11-348-413-45022	Sequence 45022, A
C 595	10	52.6	20	7	US-11-370-584-7954	Sequence 7954, Ap	C 668	10	52.6	25	9	US-11-348-413-45023	Sequence 45023, A
C 596	10	52.6	20	7	US-11-247-968A-14	Sequence 14, Appl	C 669	10	52.6	25	9	US-11-348-413-45024	Sequence 45024, A
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C 598	10	52.6	20	7	US-11-260-845-187	Sequence 187, App	C 671	10	52.6	25	9	US-11-348-413-45026	Sequence 45026, A
C 599	10	52.6	20	7	US-11-260-845-188	Sequence 188, App	C 672	10	52.6	25	9	US-11-348-413-45027	Sequence 45027, A
C 600	10	52.6	20	7	US-11-260-845-189	Sequence 189, App	C 673	10	52.6	25	9	US-11-348-413-70472	Sequence 70472, A
C 601	10	52.6	20	7	US-11-438-172-9	Sequence 9, Appli	C 674	10	52.6	25	9	US-11-348-413-70473	Sequence 70473, A
C 602	10	52.6	20	7	US-11-320-072-242	Sequence 242, App	C 675	10	52.6	25	9	US-11-348-413-70474	Sequence 70474, A
C 603	10	52.6	20	9	US-11-301-360-920	Sequence 920, App	C 676	10	52.6	25	9	US-11-348-413-70475	Sequence 70475, A
C 604	10	52.6	20	9	US-11-301-360-921	Sequence 921, App	C 677	10	52.6	25	9	US-11-348-413-70476	Sequence 70476, A
C 605	10	52.6	20	9	US-11-250-830-21	Sequence 21, Appl	C 678	10	52.6	25	9	US-11-348-413-70477	Sequence 70477, A
C 606	10	52.6	21	6	US-10-511-937-1461	Sequence 1461, Ap	C 679	10	52.6	25	9	US-11-348-413-74574	Sequence 74574, A
C 607	10	52.6	21	7	US-11-260-845-174	Sequence 174, App	C 680	10	52.6	25	9	US-11-348-413-74575	Sequence 74575, A

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742	10	52.6	25	9	US-11-348-413-614230	Sequence 614230,	C 815	10	52.6	25	9	US-11-293-024-38	Sequence 38, Appl
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747	10	52.6	25	9	US-11-348-413-663896	Sequence 663896,	C 820	10	52.6	25	9	US-11-260-845-170	Sequence 170, App
748	10	52.6	25	9	US-11-348-413-663896	Sequence 663896,	C 821	10	52.6	25	9	US-11-260-845-175	Sequence 175, App
749	10	52.6	25	9	US-11-348-413-703291	Sequence 703291,	C 822	10	52.6	25	9	US-11-260-845-185	Sequence 185, App
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751	10	52.6	25	9	US-11-348-413-711304	Sequence 711304,	C 824	10	52.6	25	9	US-11-293-598-39	Sequence 39, Appl
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ALIGNMENTS

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RESULT 1
US-10-477-471-7
, Sequence 7, Application US/10477471
, Publication No. US20060161995A1
, GENERAL INFORMATION:
, APPLICANT: Kirin Beer Kabushiki Kaisha
, TITLE OF INVENTION: Human artificial chromosomes comprising human antibody
, TITLE OF INVENTION: light chain VE gene, and non-human animals retaining
, TITLE OF INVENTION: human artificial chromosome transmittable to progeny
, FILE REFERENCE: PH-1574-PCT
, CURRENT APPLICATION NUMBER: US/10/477,471
, CURRENT FILING DATE: 2003-11-12
, PRIOR APPLICATION NUMBER: JP 2001-142371
, PRIOR FILING DATE: 2001-05-11
, NUMBER OF SEQ ID NOS: 16
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 7
, LENGTH: 30
, TYPE: DNA
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence:primer
US-10-477-471-7

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RESULT 2
US-11-320-440-213/c
; Sequence 213, Application US/11320440
; Publication No. US20060141518A1
; GENERAL INFORMATION:
; APPLICANT: Applera Corporation
; TITLE OF INVENTION: Detection of Gene Expression

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; FILE REFERENCE: 9692-000052
; CURRENT APPLICATION NUMBER: US/11/320,440
; CURRENT FILING DATE: 2005-12-28
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetically derived forward primer
US-11-320-440-213

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RESULT 3
US-11-370-584-9827/c
; Sequence 9827, Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high
; TITLE OF INVENTION: density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9827
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-7671 for SEQ 1962,
; OTHER INFORMATION: in complement
; US-11-370-584-9827

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RESULT 4
US-11-324-563-66/c
; Sequence 66, Application US/11324563
; Publication No. US20060141519A1
; GENERAL INFORMATION:
; APPLICANT: Millonig, James H.
; APPLICANT: Brzustowicz, Linda

; APPLICANT: Charani, Neda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AUTISM
; FILE REFERENCE: UMD0115US.P1
; CURRENT APPLICATION NUMBER: US/11/324,563
; CURRENT FILING DATE: 2006-01-03
; PRIOR APPLICATION NUMBER: PCT/US2004/021301
; PRIOR FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US 60/721,192
; PRIOR FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US 60/484,633
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-11-324-563-66

Query Match 66.3%; Score 12.6; DB 9; Length 21;
Best Local Similarity 78.9%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTGCT 19
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Db 21 GGAGAAGGGAGGAGGAGTT 3

RESULT 5

US-11-378-920-23/c
; Sequence 23, Application US/11378920
; Publication No. US20060218674A1
; GENERAL INFORMATION:
; APPLICANT: SAKAI, HAJIME
; APPLICANT: NAGASAWA, NORUHIRO
; TITLE OF INVENTION: ALTERATION OF PLANT EMBRYO/ENDOSPERM SIZE DURING DEVELOPMENT
; FILE REFERENCE: BB1536 US NA
; CURRENT APPLICATION NUMBER: US/11/378,920
; CURRENT FILING DATE: 2006-03-17
; PRIOR APPLICATION NUMBER: 60/664,512
; PRIOR FILING DATE: 2005-03-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer LOB F2
US-11-378-920-23

Query Match 66.3%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTGCT 19
|||||
Db 23 GGAGAAATGTTGGGAGCT 5

RESULT 6

US-10-511-937-1926
; Sequence 1926, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1926
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: 1926
US-10-511-937-1926

Query Match 64.2%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGCT 19
|||||
Db 1 AGAAGGTGGTGGCTGGT 17

RESULT 7

US-10-548-681-35/c
; Sequence 35, Application US/10548681
; Publication No. US20060166214A1
; GENERAL INFORMATION:
; APPLICANT: Yukio KATO
; APPLICANT: Koichiro TSUJI
; APPLICANT: Chika KOIKE
; TITLE OF INVENTION: Marker for detecting mesenchymal stem cell and method of distinguishing
; FILE REFERENCE: 4439-4035
; CURRENT APPLICATION NUMBER: US/10/548,681
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: JP2003-63077
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MHC Class 2 DR beta3 antisense primer
US-10-548-681-35

Query Match 64.2%; Score 12.2; DB 6; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAAGGGGGTGGGTGC 18
|||||
Db 18 GAGAACGTGGTGTGTC 2

RESULT 8

US-11-217-529-60224/c
; Sequence 60224, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO

```
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60224
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-60224
```

```
Query Match      64.2%; Score 12.2; DB 8; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 AGAAGGGGGTGGTGCT 19
      ||||| ||||| ||||| ||
DB      25 AGAAGAGGGTTGGTCT 9
```

```
RESULT 9
US-11-348-413-1052286
; Sequence 1052286, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052286
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 57; Stop 81;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052286
```

```
Query Match      64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 AGAAGGGGGTGGTGCT 19
      ||||| ||||| ||||| ||
DB      9 AAAATGGTGTGGTGCT 25
```

```
RESULT 10
US-11-348-413-1052287
; Sequence 1052287, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052287
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 58; Stop 82;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052287
```

```
Query Match      64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 AGAAGGGGGTGGTGCT 19
      ||||| ||||| ||||| ||
DB      8 AAAATGGTGTGGTGCT 24
```

```
RESULT 11
US-11-348-413-1052288
; Sequence 1052288, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052288
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 59; Stop 83;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052288
```

```
Query Match      64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```


QY 3 AGAAGGGGTGGTGCT 19
Db 7 AAAATGGTGGGTGCT 23

RESULT 12

US-11-348-413-1052289
; Sequence 1052289, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052289
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 60; Stop 84;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052289

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGTGCT 19
Db 6 AAAATGGTGGGTGCT 22

RESULT 13

US-11-348-413-1052290
; Sequence 1052290, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 65; Stop 89;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052290

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGTGCT 19
Db 1 AAAATGGTGGGTGCT 17

RESULT 14

US-11-199-903-3
; Sequence 3, Application US/11199903
; Publication No. US20060216274A1
; GENERAL INFORMATION:
; APPLICANT: Kurtzman, Gary J.
; APPLICANT: Engelman, Edgar G.
; APPLICANT: Podaskoff, Greg M.
; TITLE OF INVENTION: Induction Of Immune Response To Antigens Expressed By
; TITLE OF INVENTION: Recombinant Adeno-Associated Virus
; FILE REFERENCE: AVIGEN-03398
; CURRENT APPLICATION NUMBER: US/11/199,903
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US/09/858,728
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/121,162
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: 60/053,773
; PRIOR FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-199-903-3

Query Match 62.1%; Score 11.8; DB 7; Length 21;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGAAGGGGTGGG 15
Db 1 GGGCAAGGGGTGGG 15

RESULT 15

US-11-305-629-9
; Sequence 9, Application US/11305629
; Publication No. US20060099185A1
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
; RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/305,629
FILING DATE: 15-Dec-2005
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/10/458,857
FILING DATE: 10-Jun-2003
APPLICATION NUMBER: US/08/785,750
FILING DATE: 16-Jan-1997
APPLICATION NUMBER: US 08/598,355
FILING DATE: 18-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, Thomas P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415)325-7823
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-11-305-629-9

Query Match 62.1%; Score 11.8; DB 8; Length 21;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGAAGGGGGTGGG 15
DB 1 GGGAAGGGGGTGGG 15

RESULT 16
US-11-329-941-11
Sequence 11, Application US/11329941
Publication No. US20060104954A1
GENERAL INFORMATION:
APPLICANT: Podsakoff, Gregory
APPLICANT: Watson, Gordon
APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS FOR THE
TREATMENT OF LYSSOMAL DISORDERS
FILE REFERENCE: 0800-0021
CURRENT APPLICATION NUMBER: US/11/329,941
CURRENT FILING DATE: 2006-01-11
PRIOR APPLICATION NUMBER: US/10/421,175
PRIOR FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/09/715,858
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-11-329-941-11

Query Match 62.1%; Score 11.8; DB 8; Length 21;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGAAGGGGGTGGG 15

DB 1 GGGAAGGGGGTGGG 15
RESULT 17
US-11-348-413-635553
Sequence 635553, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 635553
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc feature
LOCATION: (1)-(25)
OTHER INFORMATION: SEQ ID NO: 806; WAN01UJOT_at; Start 593; Stop 617;
OTHER INFORMATION: 0111010000000000
US-11-348-413-635553

Query Match 62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 AGAAGGGGGTGGTG 17
DB 4 AGAAGGTGGTGGATG 18

RESULT 18
US-11-348-413-709656/c
Sequence 709656, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 709656
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
US-11-348-413-709656

```
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2889; WAN01UNF9_at; Start 82; Stop 106;
; INFORMATION: 11111100000000
US-11-348-413-709656

Query Match      62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAGGGGGTGGGTGCT 19
Db      19 AAGGGGGTGGGTGCT 5

RESULT 19
US-11-348-413-1052291
; Sequence 1052291, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 66; Stop 90;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052291

Query Match      62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAGGGGGTGGGTGCT 19
Db      2 AATGGTGTGGGTGCT 16

RESULT 20
US-11-348-413-1052292
; Sequence 1052292, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
```

```
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 67; Stop 91;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052292

Query Match      62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAGGGGGTGGGTGCT 19
Db      1 AATGGTGTGGGTGCT 15

RESULT 21
US-11-348-413-1236138
; Sequence 1236138, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1236138
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 17507; WAN01UQWB_at; Start 138; Stop 162;
; OTHER INFORMATION: 000000000000001
US-11-348-413-1236138

Query Match      62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAGGGGGTGGGTGCT 19
Db      8 AAAGGTGTGGGTGCT 22

RESULT 22
US-11-529-89292
; Sequence 89292, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
```

```
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-89292
```

```
Query Match          61.1%; Score 11.6; DB 8; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 GAGAAAGGGGTGGGTGCT 19
        ||||| ||||| ||||| |||||
Db      1 GAGAAATCCGGTGGTGTCT 18
```

```
RESULT 23
US-11-348-413-69158
; Sequence 69158, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: PCT/US05/035471
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: US 11/348,413
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 69158
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 1472; WAN01UKK4; Start 584; Stop 608;
; OTHER INFORMATION: 00100000000000
US-11-348-413-69158
```

```
Query Match          61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 GAGAAAGGGGTGGGTGCT 19
        ||||| ||||| ||||| |||||
Db      1 GAGAAAGAGGAGGTGCT 18
```

```
RESULT 24
US-11-348-413-480499
```

```
; Sequence 480499, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 480499
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14366; WAN01UQEO; Start 146; Stop 170;
; OTHER INFORMATION: 000000000001000
US-11-348-413-480499
```

```
Query Match          61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 GAGAAAGGGGTGGGTGCT 19
        ||||| ||||| ||||| |||||
Db      8 GATAATGGGATGGTGTCT 25
```

```
RESULT 25
US-11-348-413-480500
; Sequence 480500, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 480500
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14366; WAN01UQEO; Start 147; Stop 171;
; OTHER INFORMATION: 000000000001000
US-11-348-413-480500
```

```
Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
DB 7 GATAATGGGATGGTGCT 24

RESULT 26
US-11-348-413-480501
; Sequence 480501, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 480501
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14366; WAN01UQBO; Start 148; Stop 172;
; OTHER INFORMATION: 00000000001000
US-11-348-413-480501

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
DB 6 GATAATGGGATGGTGCT 23

RESULT 27
US-11-348-413-649751
; Sequence 649751, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 649751
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 1472; WAN01UKK4_at; Start 583; Stop 607;
; OTHER INFORMATION: 0010000000000000
US-11-348-413-660009

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
DB 2 GAGAAAGGAGGAGGTGCT 19

RESULT 29
US-11-348-413-783470/c
; Sequence 783470, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
```

```
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 1189; WAN01UK4Y_at; Start 177; Stop 201;
; OTHER INFORMATION: 0000100000000000
US-11-348-413-649751

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
DB 3 GAGAAAGGAGGAGGTGCT 20

RESULT 28
US-11-348-413-660009
; Sequence 660009, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 660009
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 1472; WAN01UKK4_at; Start 583; Stop 607;
; OTHER INFORMATION: 0010000000000000
US-11-348-413-660009

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
DB 2 GAGAAAGGAGGAGGTGCT 19

RESULT 29
US-11-348-413-783470/c
; Sequence 783470, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
```

```
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 783470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 5091; WAN01PAAQ_at; Start 112; Stop 136;
; OTHER INFORMATION: 000001000000000
US-11-348-413-783470
```

```
Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 2 GAGAGGGGGTGGTGCT 19
    ||||| ||| ||| |||
Db 23 GAGAGGGTGGTGGCTGT 6
```

```
RESULT 30
US-11-348-413-783471/c
; Sequence 783471, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 783471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 5091; WAN01PAAQ_at; Start 115; Stop 139;
; OTHER INFORMATION: 000001000000000
US-11-348-413-783471
```

```
Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 2 GAGAGGGGGTGGTGCT 19
    ||||| ||| ||| |||
Db 20 GAGAGGGTGGTGGCTGT 3
```

RESULT 31

```
US-11-348-413-783472/c
; Sequence 783472, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 783472
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 5091; WAN01PAAQ_at; Start 117; Stop 141;
; OTHER INFORMATION: 000001000000000
US-11-348-413-783472
```

```
Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 2 GAGAGGGGGTGGTGCT 19
    ||||| ||| ||| |||
Db 18 GAGAGGGTGGTGGCTGT 1
```

RESULT 32

```
US-11-348-413-1225381
; Sequence 1225381, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1225381
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 17229; WAN01UQN2_at; Start 349; Stop 373;
; OTHER INFORMATION: 0000000000001100
```

US-11-348-413-1225381

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
DB 1 GACAACGGGTGATGCT 18

RESULT 33
US-11-260-845-310/c
; Sequence 310, Application US/11260845
; Publication No. US20060183207A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamicheva, Natasha
; TITLE OF INVENTION: FEN Endonucleases
; FILE REFERENCE: FORS-09451
; CURRENT APPLICATION NUMBER: US/11/260,845
; CURRENT FILING DATE: 2005-11-27
; NUMBER OF SEQ ID NOS: 410
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 310
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Archaeoglobus veneficus
US-11-260-845-310

Query Match 61.1%; Score 11.6; DB 7; Length 27;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGAGGGGGTGGTGCT 18
DB 22 GGAGAGGTGATCGTGC 5

RESULT 34
US-11-368-233-179/c
; Sequence 179, Application US/11368233
; Publication No. US20060205040A1
; GENERAL INFORMATION:
; APPLICANT: Sampath, Rangarajan
; TITLE OF INVENTION: COMPOSITIONS FOR USE IN IDENTIFICATION OF ADVENTITIOUS VIRUSES
; FILE REFERENCE: DIBS-0085US1 (10774)
; CURRENT APPLICATION NUMBER: US/11/368,233
; CURRENT FILING DATE: 2006-03-03
; PRIOR APPLICATION NUMBER: 60/658,248
; PRIOR FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: 60/705,631
; PRIOR FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: 60/732,539
; PRIOR FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/740,617
; PRIOR FILING DATE: 2005-11-28
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: PatentIn Ver. 4.0
; SEQ ID NO 179
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-368-233-179

Query Match 61.1%; Score 11.6; DB 7; Length 28;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19

DB 26 GAGAATGGGTGGGCCT 9

RESULT 35
US-11-368-233-180/c
; Sequence 180, Application US/11368233
; Publication No. US20060205040A1
; GENERAL INFORMATION:
; APPLICANT: Sampath, Rangarajan
; TITLE OF INVENTION: COMPOSITIONS FOR USE IN IDENTIFICATION OF ADVENTITIOUS VIRUSES
; FILE REFERENCE: DIBS-0085US1 (10774)
; CURRENT APPLICATION NUMBER: US/11/368,233
; CURRENT FILING DATE: 2006-03-03
; PRIOR APPLICATION NUMBER: 60/658,248
; PRIOR FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: 60/705,631
; PRIOR FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: 60/732,539
; PRIOR FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/740,617
; PRIOR FILING DATE: 2005-11-28
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: PatentIn Ver. 4.0
; SEQ ID NO 180
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (24)...(24)
; OTHER INFORMATION: I
US-11-368-233-180

Query Match 61.1%; Score 11.6; DB 7; Length 28;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
DB 26 GAGAATGGGTGGGCCT 9

RESULT 36
US-11-217-936-4208/c
; Sequence 4208, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4208
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-4208

Query Match 60.0%; Score 11.4; DB 9; Length 19;
Best Local Similarity 92.3%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 6 AGGGGGTGGTGC 18
Db 18 AGGGGGTGGTGC 6

RESULT 37
US-11-217-936-4466
; Sequence 4466, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siRNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4466
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-4466

Query Match 60.0%; Score 11.4; DB 9; Length 19;
Best Local Similarity 76.9%; Pred. No. 4.1e+04;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGGGGGTGGTGC 18
Db 2 AGGGGGUUGGUGC 14

RESULT 38
US-11-316-132-25
; Sequence 25, Application US/11316132
; Publication No. US20060100153A1
; GENERAL INFORMATION:
; APPLICANT: Shridhar, Vijai
; APPLICANT: Roberts, Lewis R.
; APPLICANT: Kaufmann, Scott H.
; TITLE OF INVENTION: Hsulf-1 Nucleic Acids, Polypeptides and
; TITLE OF INVENTION: Methods of Using
; FILE REFERENCE: 07039/449001
; CURRENT APPLICATION NUMBER: US/11/316,132
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/778,607
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/446,945
; PRIOR FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-316-132-25

Query Match 60.0%; Score 11.4; DB 8; Length 20;
Best Local Similarity 92.3%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGGGGGTGGTGC 18
Db 2 AGAGGGTGGTGC 14
```

```
RESULT 39
US-10-818-956-78/c
; Sequence 78, Application US/10818956
; Publication No. US20060134639A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; APPLICANT: Zammattéo, Nathalie
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
; FILE REFERENCE: KLAUS2.006AUS
; CURRENT APPLICATION NUMBER: US/10/818,956
; CURRENT FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-818-956-78

Query Match 60.0%; Score 11.4; DB 6; Length 22;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTG 13
Db 15 GGAGAGGTGGTG 3

RESULT 40
US-11-317-660-380/c
; Sequence 380, Application US/11317660
; Publication No. US20060185027A1
; GENERAL INFORMATION:
; APPLICANT: BARTEL, DAVID P.
; APPLICANT: JONES-RHOADES, MATTHEW W.
; APPLICANT: LEWIS, BENJAMIN P.
; APPLICANT: BURGE, CHRISTOPHER B.
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR IDENTIFYING MIRNA TARGETS
; TITLE OF INVENTION: AND FOR ALTERING MIRNA AND TARGET EXPRESSION
; FILE REFERENCE: W0571.70013US01
; CURRENT APPLICATION NUMBER: US/11/317,660
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: 60/639,231
; PRIOR FILING DATE: 2004-12-23
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 380
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-317-660-380

Query Match 60.0%; Score 11.4; DB 7; Length 22;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTG 13
Db 15 GGAGAGGTGGTG 3

RESULT 41
US-11-317-660-1139
; Sequence 1139, Application US/11317660
; Publication No. US20060185027A1
; GENERAL INFORMATION:
```



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; APPLICANT: BARTEL, DAVID P.
; APPLICANT: JONES-BROADEN, MATTHEW W.
; APPLICANT: LEWIS, BENJAMIN P.
; APPLICANT: BURGE, CHRISTOPHER B.
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR IDENTIFYING MIRNA TARGETS
; FILE REFERENCE: W0571.70013US01
; CURRENT APPLICATION NUMBER: US/11/317,660
; PRIOR FILING DATE: 2005-12-23
; PRIOR FILING DATE: 2004-12-23
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1139
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-317-660-1139

Query Match          60.0%; Score 11.4; DB 7; Length 22;
Best Local Similarity 84.6%; Pred. No. 4.2e+04;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GGAGAAGGGGGTGG 13
        |||||
Db      8  GGAGAAGGGUGG 20

RESULT 42
US-11-242-139-94/c
; Sequence 94, Application US/11242139
; Publication No. US20060099619A1
; GENERAL INFORMATION:
; APPLICANT: REMACLE, JOSE
; APPLICANT: DU LONGUEVILLE, FRANCOISE
; APPLICANT: HAMELS, SANDRINE
; TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF MIRNA ON MICRO-ARRAYS
; FILE REFERENCE: 035642-0107
; CURRENT APPLICATION NUMBER: US/11/242,139
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: 10/637,656
; PRIOR FILING DATE: 2003-08-11
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-242-139-94

Query Match          60.0%; Score 11.4; DB 8; Length 22;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GGAGAAGGGGGTGG 13
        |||||
Db      15 GGAGAAGGGTGG 3

RESULT 43
US-11-283-550-1462/c
; Sequence 1462, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
```

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; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1462
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1462

Query Match          60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3  AGAAGGGGGTGGG 15
        |||||
Db      23 AGAAGGGGGTTGG 11

RESULT 44
US-11-283-550-1463/c
; Sequence 1463, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1463
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1463

Query Match          60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3  AGAAGGGGGTGGG 15
        |||||
Db      22 AGAAGGGGGTTGG 10

RESULT 45
US-11-283-550-1464/c
; Sequence 1464, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
```

; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1464
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1464

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGG 15
|||||
Db 21 AGAAGGGGGTGGG 9

RESULT 46
US-11-283-550-1465/c
; Sequence 1465, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1465
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1465

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGG 15
|||||
Db 20 AGAAGGGGGTGGG 8

RESULT 47

US-11-283-550-1466/c
; Sequence 1466, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1466
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1466

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGG 15
|||||
Db 19 AGAAGGGGGTGGG 7

RESULT 48
US-11-283-550-1467/c
; Sequence 1467, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1467
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1467

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGG 15

Db 18 AGAAGGGGGTTGG 6
|||||||

RESULT 49
US-11-283-550-1468/c
; Sequence 1468, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biopharmaceuticals, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1468
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1468

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTTGG 15
|||||||

Db 17 AGAAGGGGGTTGG 5
|||||||

RESULT 50
US-11-283-550-1469/c
; Sequence 1469, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biopharmaceuticals, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1469
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1469

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTTGG 15
|||||||

Db 16 AGAAGGGGGTTGG 4
|||||||

Search completed: October 14, 2006, 20:26:48
Job time : 133 secs

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